

* * *

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:48:09 1996; MasPar time 264.75 Seconds
1018.838 Million cell updates/sec

Tabular output not generated.

Title: >US-08-137-117B-28

Description: (1-381) from US08137117B.seq

Perfect Score: 381
 N.A. Sequence: 1 ATGGTGTCTCAGTCACTT.....GGACCAAGCTGGAATAAAT 381
 Comp: TACCACAGAGGTCAGTCAA.....CCTGTTTCGACCTTTATTTA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 264399 seqs. 353985056 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: embl-new11

1: BCT 2: FUN 3: INV1 4: INV2 5: INV3 6: MAM 7: ORG 8: PIN
9: PRI1 10: PRI2 11: PRI3 12: PRO1 13: PRO2 14: ROD 15: SYN
16: UNC 17: VRT 18: VIR

Database: aenbank91

19:BC11 20:BC12 21:BC13 22:BC14 23:BC15 24:BC16 25:BC17
26:IN11 27:IN12 28:IN13 29:IN14 30:IN15 31:MAM1 32:MAM2
33:PA11 34:PA12 35:PA13 36:PHG 37:PLN1 38:PLN2 39:PLN3
40:PLN4 41:PLN5 42:PLN6 43:PLN7 44:PR11 45:PR12 46:PR13
47:PR14 48:PR15 49:PR16 50:PR17 51:PR18 52:PR19 53:ROD1
54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD6 59:ROD7 60:STR
61:SYN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5
68:VRL6 69:VRT1 70:VRT2 71:VRT3

Database:

72:BCT1 73:BCT2 74:INV1 75:INV2 76:NAM 77:PHG 78:PLN
79:PRI1 80:PRI2 81:PRI3 82:ROD 83:STR 84:SYN 85:UNA

Database: u-emb144 91

88:part1

Statistics: Mean 10.298; Variance 3.799; scale 2.711

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	354	92.9	381.59	S50261	Ig VL-anti-CD4 mAb M-	0.00e+00
2	354	92.9	393.56	MUSIVJR	Mus musculus germline	0.00e+00
3	352	92.4	395.56	MUSIGKAAAL	Mouse Ig kappa chain	0.00e+00
4	350	91.9	381.14	MM16689	Mus musculus Ig light	0.00e+00
5	350	91.9	381.82	MM16689	Mus musculus Ig light	0.00e+00
6	344	90.3	381.54	MMU05217	Mus musculus Balb/c a	0.00e+00
7	343	90.0	378.56	MUSIGK527A	Mus musculus (clone 5	0.00e+00
8	336	88.2	366.56	MUSIGKCKO	Mouse Ig kappa-chain	0.00e+00
9	328	86.1	345.56	MUSIGKCPW	Mouse Ig active kappa	0.00e+00
10	316	82.9	395.56	MUSIGKAAAM	Mouse Ig kappa chain	0.00e+00
11	310	81.4	324.56	MUSIGKAVD	Mouse Ig rearranged k	0.00e+00
12	310	81.4	324.54	MMIGKL229	M.musculus gene for i	0.00e+00
13	310	81.4	324.54	MMIGKL38	M.musculus gene for i	0.00e+00
14	310	81.4	324.54	MMIGKL233	M.musculus gene for i	0.00e+00
15	310	81.4	324.56	MUSIGKAVF	Mouse Ig rearranged k	0.00e+00
16	310	81.4	324.56	MUSIGKAVE	Mouse Ig rearranged k	0.00e+00
17	308	80.8	408.59	SE3072	anti-ganglioside GD3	0.00e+00
18	302	79.3	508.53	MMS52H1VL	M.musculus/ H.sapiens	4.71e-300
19	298	78.2	324.54	MMIGLIC151	M.musculus mRNA for I	1.68e-295
20	298	78.2	324.54	MMIGKLAB0	M.musculus gene for i	1.68e-295
21	298	78.2	324.54	MMIGKLAC1	M.musculus gene for i	1.68e-295
22	298	78.2	324.56	MUSIGKAVA	Mouse Ig rearranged k	1.68e-295
23	298	78.2	324.56	MUSIGKAVH	Mouse Ig rearranged k	1.68e-295
24	298	78.2	324.54	MMIGKL218	M.musculus gene for i	1.68e-295
25	298	78.2	324.54	MUSIGKAVJ	Mouse Ig rearranged k	1.68e-295
26	296	77.7	330.54	MMU08020	Mus musculus Ig Fab F	3.18e-293
27	295	77.4	321.54	MMNL4H10	M.musculus NL4H10 mRN	4.37e-292
28	294	77.2	321.56	MUSIGKJ	Mouse Ig kappa germli	6.00e-291
29	294	77.2	321.56	MUSIGKADT	Mouse Ig rearranged k	6.00e-291
30	294	77.2	323.54	MMIGVK36	Mouse hybridoma 36-65	6.00e-291
31	294	77.2	323.56	MUSIGKABT	Mouse Ig kappa-chain	6.00e-291
32	294	77.2	324.56	MUSIGKCOD	Mouse Ig active kappa	6.00e-291
33	294	77.2	324.56	MUSIGKAVC	Mouse Ig rearranged k	6.00e-291
34	294	77.2	324.56	MUSIGKCRS	Mouse Ig kappa-chain	6.00e-291
35	294	77.2	324.56	MUSIGKAAO	Mouse Ig kappa active	6.00e-291
36	294	77.2	324.54	MMIGKL228	M.musculus gene for i	6.00e-291
37	294	77.2	324.56	MUSIGKCR	Mouse Ig kappa-chain	6.00e-291
38	294	77.2	324.56	MUSIGKCOB	Mouse Ig active kappa	6.00e-291
39	294	77.2	324.56	MUSIGKCP	Mouse Ig kappa-chain	6.00e-291
40	294	77.2	324.56	MUSIGKCO	Mouse Ig active kappa	6.00e-291
41	294	77.2	324.56	MUSIGKCT	Mouse Ig active kappa	6.00e-291
42	293	76.9	324.56	MUSIGKCT	Mouse Ig kappa-chain	8.23e-290
43	293	76.9	324.56	MUSIGKCRQ	Mouse Ig kappa-chain	8.23e-290
44	292	76.6	321.53	MMIGLIAQ	Mouse Ig light-chain	1.13e-288
45	292	76.6	324.53	MUSIGP68	M.musculus gene for I	1.13e-288

ALIGNMENTS

RESULT	1
LOCUS	S50261 381 bp mRNA ROD 02-APR-1993
DEFINITION	Ig VL=anti-CD4 mAb M-T151 variable region light chain [J2, chimeric antibody] [mice, hybridoma cells, mRNA partial, 381 nt].
ACCESSION	S50261
KEYWORDS	.
SOURCE	mice hybridoma cells.
ORGANISM	Mus sp. Unclassified.


```

|||||
Qy 241 AGGTTGAGTGGCAGTGGCTGGACAGATATTCTCTACCAATTAAACAACCTGGAGCAA 300
Db 301 gaagatatggcaactattcttggcaacagggttaatacgttcctgagcgttcggtgga 360
Qy 301 GAAGACATTGCCATTACTTTTCCCAACAGGTAACACAGCTTCCGTCACAGCTTCGGAGG 360
Db 361 ggcaccaagctggaatacaa 380
Qy 361 GCGACCAAGCTGGAATAAA 380

RESULT 3
LOCUS MUSICKAAL 395 bp mRNA ROD 29-OCT-1994
DEFINITION Mouse Ig kappa chain mRNA V-J region, 5' end.
ACCESSION M60019
KEYWORDS C-region; J-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa.
SOURCE Mouse (strain C57BL/6) spleen cell hybridoma 244, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Euthera; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 395)
AUTHORS Brigid, M.M. and Stollar, B.D.
TITLE Two induced anti-2-DNA monoclonal antibodies use VH gene segments
related to those of anti-DNA autoantibodies
JOURNAL J. Immunol. 146 (6), 2005-2009 (1991)
MEDLINE 91170743
COMMENT NCBI gi: 196423
FEATURES
    Location/Qualifiers
        source
            1..395
                /organism="Mus musculus"
                /cell_line="hybridoma 244"
                /dev_stage="fetus"
                /sequenced_mol="cDNA to mRNA"
                /tissue_type="Liver"
sig_peptide 12..71
            /gene="IgM"
            /map="chromosome 6"
            /codon_start=1
CDS 12..395
    /partial
    /gene="IgM"
    /map="chromosome 6"
    /note="NCBI gi: 196424"
    /codon_start=1
    /product="Ig kappa chain"
    /translation="MSSAQFLGILLCTQGRCDQFQMTTSSLSASLGDRVTSR
ASQDINLWYQKQKDGTKLLIYTSILHSGVPARFSGSGSGTYSLIINLEQD
IATVFCQGNLTPTTFGGSKLEIKR"
V_region 72..356
    /gene="IgM"
    /map="chromosome 6"
mat_peptide 72..395
    /gene="IgM"
    /map="chromosome 6"
    /codon_start=1
    /product="Ig kappa chain"
    /note="357..395"
J_segment 357..395
    /gene="IgM"
    /map="chromosome 6"
BASE COUNT 105 a 96 c 90 g 104 t
ORIGIN Chromosome 6.
```

```

Query Match 92.4%; Score 352; DB 56; Length 395;
Best Local Similarity 96.3%; Pred. No. 0.00e+00;
Matches 366; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 12 atgatatctctgctcagtcctctggtgtctcctgtgtctgtctgttttcaaggtaccagatgt 71
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 ATGGTGCTCTCAGCTCAGTCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60

Db 72 gattccagatgacgacagactacatcctcctgtctgctctctctgggagacagagtcaacc 131
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 GATATCCAGATCACACAGACTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

Db 132 atcagttgcagggtcaagtcaggacattagcaattatttaaaactggtatcagcagaaccaa 191
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 ATCAGTTGCGAGGCACTAGCAGATACAGATATTAACTGATATTAACTGATATTAACTGATAT 180

Db 192 gatggaactgttaaaactcctgatctactacacatcaatatttaaaactggtatcagcaga 251
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 CATGGAACATATTAAACTCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240

Db 252 aggttcagtcgagtcgggtctggaacagattatctctcattcattcattcattcattcattc 311
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 AGGTTGAGTGGCAGTGGCTGGAAACAGATATTCTCTCACCATTAAACAACCTGGAGCAA 300

Db 312 gaagatatggcaactattcttggcaacagggttaacacgcttcctcattcattcattcattc 371
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 GAAGACATTGCCACTTACTTTTCCCAACAGGTAACAGCTTCCGTCACAGCTTCGGAGGG 360

Db 372 gggccaagctgggaataaa 391
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 361 GCGACCAAGCTGGAATAAA 380

RESULT 4
ID MM16689 standard; RNA; ROD; 381 BP.
AC U16689;
DT 03-NOV-1995 (Rel. 45, Created)
DT 03-NOV-1995 (Rel. 45, Last updated, Version 1)
DE Mus musculus Ig light chain leader and variable region Vk V gene
family mRNA, partial cds.
KW .
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Euthera; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-381
RA White K.D., Frank M.B., Foundling S., Cummings R.D., Waxman F.J.;
RT "Effect of variable domain structure and CH2-linked carbohydrate
on C3b and C4b deposition and classical complement pathway
activation by immunoglobulins";
RL Unpublished.
RN [2]
RP 1-381
RA Frank B.;
RT ;
Submitted (27-OCT-1994) to the EMBL/GenBank/DBJ databases.
RL Bart Frank, Arthritis and Immunology Program, Oklahoma Medical
Research Foundation, 825 NE 13th Street, Oklahoma City, OK 73104,
USA
CC NCBI gi: 1041800
FH Key Location/Qualifiers
FH source 1..381
FT /clone="10/131CIF7"
FT
```

```

FT      /strain="BALB/c"
FT      /organism="Mus musculus"
FT      /sex="female"
FT      /cell_type="hybridoma (NS-1 x spleen cells) post DNP-BSA
FT      immunizations"
FT      1..>381
FT      CDS
FT      /note="NCBI gi: 1041801"
FT      /codon_start=1
FT      /product="immunoglobulin light chain precursor"
FT      /note="pid:gi1041801"
FT      1..60
FT      sig_peptide
FT      /note="leader region"
FT      61..324
FT      misc_feature
FT      /note="encodes R1 through FR3 of immunoglobulin V-kappa"
FT      V_region
FT      61..381
FT      /note="member of the murine Vk V gene family"
FT      /product="immunoglobulin light chain variable region"
FT      346..381
FT      J_segment
FT      /note="Jk1 encoded residues"
FT      Sequence 381 BP: 105 A; 92 C; 83 G; 101 T; 0 other;
SQ

```

Query Match	91.9%;	Score 350;	DB 14;	Length 381;
Best Local Similarity	96.1%;	Pred. No. 0.00e+00;		
Matches 365;	Conservative 0;	Mismatches 15;	Indels 0;	Gaps 0;

1	atgatgctcctctgctcagttcccttgctcctggtgctctctgtgtttccaaggtaccagatgt	60
1	ATGGTGCTCTCAGCTCAGTTCCTTGGTCTCCTTGCTCTGTGTTTTCAAGGTACCAGATGT	60
61	gatccagatgacacagactacatccctctgtctcctctctggtggagacaggtcacc	120
61	GATATCCAGATGACACAGACTACATCCTCCCTCTCTGCCCTCTCTGGGACACAGTCCACC	120
121	atcagttgcagggcgaagtccaggtattagcaattatttaaactgggtatcagcagaaccca	180
121	ATCAGTTGCAGGGCGAAGTCAGGACATTAGCAGTTATTAAACTGGGTATCAGCAGAAACCA	180
181	gatggaactgttaaacctcctgatctactacacatcaagattacactcaggagtcaccatca	240
181	GATGGAACATTAAACTCTGATCTACTACATCAAGATTACTCAGGAGTCCCATCA	240
241	aggttcadtggcagtggtctggaacagattatctcaccattagcaacctggaaaca	300
241	AGGTTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAAACAACCTGGAGCAA	300
301	gaagatatggccacttactttggcaacagggtaaatcgcttcctggacgttcggtgga	360
301	GAGACATTGGCAGTTACTTTTGGCAACAGGGTAACAGGTTCCGCTACACGTTCCGAGGG	360
361	ggcaccacagctggaaalcaa	380
361	GGGACCAAGCTGGAAATAAA	380

RESULT	5
LOCUS	MWU16689 381 bp mRNA ROD 28-OCT-1995
DEFINITION	Mus musculus Ig light chain leader and variable region Vk gene family mRNA, partial cds.
ACCESSION	U16689
KEYWORDS	.
SOURCE	mouse.
ORGANISM	Mus musculus Eukaryotae; Mitochondria; Eukaryote crown group; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia;

Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia; Sciurognathi; Myomorpha; Muridae; Mus.

1 (bases 1 to 381)

White, K.D., Frank, M.B., Foundling, S., Cummings, R.D. and Waxman, F.O.

Effect of variable domain structure and CH2-linked carbohydrate on C3b and C4b deposition and classical complement pathway activation by immunoglobulins

Unpublished

2 (bases 1 to 381)

Frank, B.

Direct Submission

Submitted (27-OCT-1994) Bart Frank, Arthritis and Immunology Program, Oklahoma Medical Research Foundation, 825 NE 13th Street, Oklahoma City, OK 73104, USA

COMMENT	NCBI gi: 1041800
FEATURES	Location/Qualifiers
source	1..381

```

/organism="Mus musculus"
/sex="female"
/cell_type="hybridoma (NS-1 x spleen cells) post DNP-BSA
immunizations"

```

```
CDS
1..>381
/note="NCBI gi: 1041801"
/codon_start=1
```

```
sig_peptide      1..60      /note="leader region"
misc feature     61..324
```

```
V_region
61...381
/note="member of the murine Vk V gene family"
/product="immunoglobulin light chain variable region"
```

```

BASE COUNT      105 a      92 c      83 g      101 t
ORIGIN

```

Query Match 91.9%; Score 350; DB 82; Length 381;
Best Local Similarity 96.1%; Pred. No. 0.00e+00;
Matches 365; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

D_b 1 atgatgtctctgctcagttcccttgcctcctggttgctctgctctggttcgaaggtagaccagatgt 60
||| ||||||| |

Qv 1 ATGSGTGCTCCAGCTCAGTTCCTGGTGTCTCCTGTTGCTGTTTTCAAGGTACCAGATGT 60
||| ||||||| |

Db . 61 gatattccagatgacacagactacatcctccctgtctgcctctctggagacagagtccc 120
|||||
Ov 61 GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGACACAGACTACC 120

[illegible]

Db 181 gatggaactgttaactcctgatctactacatcaagattacactcaggagtcacatca 240

Db	241	aggdtcagtggcagtgggctggaacagattattctctcaaccattagcaaacctggaaaca	300
Qy	241	AGSTTCAGTGGCACTGGGTCTGGACAGATTATTCTCTCACCATTAAACAACCTGGACAA	300
Db	301	gaagatatggccacttaactttgccacagggtaataagcttcogtggagcgttcogtggga	360
Qy	301	GAAGACATTGCCACTTACTTTTCCCAACAGGGTAACACGGTTCCTGTACACGTTCCGAGGG	360
Db	361	ggcaccaagctggaaataca	380
Qy	361	GGGACCAAGCTGGGAATAAA	380

RESULT		6	
LOCUS	MU05217	381 bp	mRNA ROD 20-MAY-1994
DEFINITION	Mus musculus Balb/c anti-platelet integrin gpIIb/IIIa light chain immunoglobulin, partial cds.		
ACCESSION	U05217		
KEYWORDS	.		
SOURCE	mouse.		
ORGANISM	Mus musculus		
	Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;		
	Eutheria; Rodentia; Myomorpha; Muridae; Mus.		

REFERENCE	1 (sites)
AUTHORS	Co.M., Yano, S., Hsu, R.K., Landolfi, N.F., Vasquez, M., Cole, M.S., Teo, J.T., Bringman, T., Laird, W., Hudson, D., Kawamura, K. and Suzuki, K.
TITLE	A humanized antibody specific for the platelet integrin gpIb/IIIa
JOURNAL	J. Immunol. 152, 2968-2976 (1994)
MEDLINE	94194058
REFERENCE	2 (bases 1 to 381)
AUTHORS	Co.M.
TITLE	Direct Submission
JOURNAL	Submitted (14-JAN-1994) Man Sung Co. Protein Design Labs., Inc., 2375 Garcia Ave, Mountain View, CA 94043, USA
COMMENT	NCBI gi: 460600
FEATURES	Location/Qualifiers

```

source      1..381
/organism="Mus musculus"
/strain="Balb/c"
/cell_line="C4G1"
/cell_type="hybridoma"
1..60
sig_peptide
CDS        1..>381
/note="NCBI gi: 460601"
/codon_start=1
/product="anti-platelet integrin gpIb/IIIA light chain
immunoglobulin"
/translation="MWSAQFLGFLLLCFQGTGCDIQMTTSSLSASLGDRTVTSICR
ASQDINNYLAWTQQKPCGVKLLIYYTSTLHSGVPSRFSGSGSGDYSLTISNLEQDEN
IATYFCQGGNTLPWFGGGFKLEIK"
mat_peptide 61..>381
BASE COUNT 104 a 92 c 83 g 102 t
ORIGIN

```

Query Match 90.3%; Score 344; DB 54; Length 381;
Best Local Similarity 95.3%; Pred. No. 0.00e+00;
Matches 362; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy	61	GATATCCAGATGACACAGACATACCTCCCTCTCTGGGAGACAGATCACC	120
Db	121	atcagttgcagggcaggtcaggacattacaattattttaactggtatcagcagaacca	180
Qy	121	ATCAGTTCGACGGCAGATCAGGACATATGACGATTATTAAACTGGTATCAGACGAACA	180
Db	181	gatggaattgtaaactctgatctactacacacaacattaacctcaggagttcccatca	240
Qy	181	GATGGAACATTAAACTCCTCATCTACTACACACAAGATTACATCTCAGAGTCCCATCA	240
Db	241	aggttcagtggcagtggtgtggacagagattattctctcacattagcaacctggagcag	300
Qy	241	AGGTTTCAGTGGCAGTGGGTCTGGAAACAGATTATTCTCTCCACATTAAACAACCTGGAGAA	300
Db	301	gaagatatggcaacttactttggccaacagggttaatacgtctccgtggacgttcggtgga	360
Qy	301	GAAGACATTGGCACTTACTTTTGGCAACAGGGTAACAGGCTTCCTGTACACGTTTCGAGGG	360
Db	361	ggcaccacaggtggaaatcaa	380
Qy	361	GGGACCAAGCTGGAAATAAA	380

ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
1 (sites)
AUTHORS Bedzyk, W.D., Herron, J.N., Edmundson, A.B. and Voss, E.W. Jr.
TITLE Active site structure and antigen binding properties of
idiotypically cross-reactive anti-fluorescein monoclonal antibodies
J. Biol. Chem. 265 (1), 133-138 (1990)

MEDLINE	90094387
COMMENT	NCBI gi: 639666
FEATURES	Location/Qualifiers
source	1..378
	/organism="Mus musculus"
	/strain="BALB/c"
	/sub_species="domesticus"
	/cell_line="splenocyte/nonsecreting Sp2/O-Ag14 fusion cell line"
	/sequenced_mol="cDNA to mRNA"

sig peptide

CDS

```

/gene="Iqk"
/ncbi="639667"

```

```

/codon_start=1
/product="anti-fluorescein antibody"

```

product = anti-fluorescein antibody
/translation = "MSSAQLGLLLLCFGQTRCDIQMTQTSSLSASIGDRVTVSCRA
SQDINNYLWVQQKPDGTWKLIMVYTSKLHGVPSRFSGSGSGTDYSLTISNLEQEDII
ATYFCQGNLTPWFEGGGTKLEIN"

Jul 8 08:42

US-08-137-117B-28.rgs

13

different antigen (phoxazolone, NP or GAT)
JOURNAL Mol. Immunol. 25, 859-865 (1988)
MEDLINE 89096973
COMMENT NCBI gi: 197161
FEATURES Location/Qualifiers
source 1..345
/organism="Mus musculus"
sig_peptide <1..18
/note="Ig kappa-chain signal peptide"
/codon_start=1
197162
/note="Ig kappa-chain V-J region precursor; NCBI gi:
197162"
/codon_start=1
/translation="FQGTCDIQMTQTSSLSASLGDRVTISCRASQDISNYLNWQQ
KPDGTVKLIYYTSRLHSGVPSRFSGSGDYSLTISNLEQEDIATYFCQGNLTIPY
TFGGCTKLEIKRA"
19..>345
mat_peptide
/note="Ig kappa-chain V-J region"
/codon_start=1
BASE COUNT 103 a 82 c 78 g 82 t
ORIGIN

Query Match 86.1%; Score 328; DB 56; Length 345;
Best Local Similarity 98.5%; Pred. No. 0.00e+00;
Matches 333; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 1 tttaaggtaccagatgtgatcatcagatgacacagactacatccctcgtcgtcctct 60
|||||
Qy 43 TTTCAGGTACAGATGTGATATCAGATCACAGACTACATCCTCCTGCTGCCTCT 102
|||||
Db 61 ctggagacagagtcaccatcagttcaggccaagtcaggacattagcaattattaaac 120
|||||
Qy 103 CTGGGACAGAGTCACCATCAGTTGACGGGCAAGTCAGGACATTAGCAGTTATTAAAC 162
|||||
Db 121 tggatcagcagaaccagatggaactgttaactcctgatctactacacatcaagatta 180
|||||
Qy 163 TGGTATCAGCAGAACACAGATGGAACTATTAAACTCTCTGATCTACTACATCAAGATTA 222
|||||
Db 181 cactcagagtcaccatcaaggttcagtcagtcagggtctggaacagattattctcacc 240
|||||
Qy 223 CACTCAGAGTCCCATCAAGTTTCAGTGGCAGTGGGTCTGGAAACAGATTATTCTCTCACC 282
|||||
Db 241 attagcaacctggagcaagaagatattgccacttacttttggcaacagggtaatacgttt 300
|||||
Qy 283 ATTAACAACCTGGAGCAAGACATTCGCCACTTACTTTTGGCAACAGGGTAACAGCGTT 342
|||||
Db 301 cagtcacagtcggagggggggaccagctggaaataaa 338
|||||
Qy 343 CGGTACAGCTTCGGAGGGGGACCAAGCTGCAATAAA 380
|||||

RESULT 10
LOCUS MUSIGKAAAM 395 bp mRNA ROD 29-OCT-1994
DEFINITION Mouse Ig kappa chain mRNA V-J region, 5' end.
ACCESSION M60020
KEYWORDS C-region; J-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa.
SOURCE Mouse (strain C57BL/6) spleen cell hybridoma 222, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Thoria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 395)
AUTHORS Brigido, M.M. and Stollar, B.D.

Jul 8 08:42

US-08-137-117B-28.rgs

14

TITLE Two induced anti-2-DNA monoclonal antibodies use VH gene segments
related to those of anti-DNA autoantibodies
JOURNAL J. Immunol. 146 (6), 2005-2009 (1991)
MEDLINE 91170743
COMMENT NCBI gi: 196425
FEATURES Location/Qualifiers
source 1..395
/organism="Mus musculus"
/cell_line="hybridoma 222"
/dev_stage="fetus"
/sequenced_mol="cDNA to mRNA"
/tissue_type="liver"
12..71
sig_peptide
/gene="IgM"
/map="chromosome 6"
/codon_start=1
12..395
/partial
/gene="IgM"
/map="chromosome 6"
/note="NCBI gi: 196426"
/codon_start=1
/product="Ig kappa chain"
/translation="WMSSAOFGLLLLCFOCTRCDIQMTQTSSLSASLGDRVTISGS
ASGQISNYLNWQQKPDGTGTVKLIYYTSRLHSGVPSRFSGSGCTDYSLTISNLEPED
IATYFCQYQYSKFFTFGSGTKLEIKR"
72..356
V_region
/gene="IgM"
/map="chromosome 6"
72..395
/gene="IgM"
/map="chromosome 6"
/codon_start=1
/product="Ig kappa chain"
357..395
J_segment
/gene="IgM"
/map="chromosome 6"
BASE COUNT 105 a 94 c 86 g 110 t
ORIGIN Chromosome 6.

Query Match 82.9%; Score 316; DB 56; Length 395;
Best Local Similarity 91.6%; Pred. No. 0.00e+00;
Matches 348; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
Db 12 atgatgtcctctgtcagttcctcgtcctcgtctcgtctgtctgttttcaagggtaccagatgt 71
|||||
Qy 1 ATGGTGTCTCAGTCAGTTCCTGGTCTCCTGCTGCTGCTGCTTTTCAAGGTACAGATGT 60
|||||
Db 72 gatcatcagatgacacagactacatcctcctcgtcctcgtcctcgtcctcgtcctcgtcctcacc 131
|||||
Qy 61 GATATCCAGATCACAGACTACATCCTCCCTGCTCCCTCTCTGGGAGACAGAGTCAACC 120
|||||
Db 132 atcagttcagtgcaagtcaggcattagtaattatttaaaactggtatcagcagaatacca 191
|||||
Qy 121 ATCAGTTGACGGGCAAGTCAGGACATTAGCAGTTATTAACTGGTATCAGCAGAAACCA 180
|||||
Db 192 gatggaactgttaaacctcctgatctattacacatcaagattacactcagaggtcccatca 251
|||||
Qy 181 GATCGAACTATTAAACTCCTGATCTACTACATCAAGATTACTCAGGAGTCCCATCA 240
|||||
Db 252 aggttcagttggcagtggtctgggagacagattattctcaccatcagcaacctggaaacct 311
|||||
Qy 241 AGGTTCAAGTGGCAGTGGGTCTGGAAACAGATTATTCTCTCACCATTAAACACCTGGAGCAA 300
|||||

Jul 8 08:42

US-08-137-117B-28.rgs

15

```

Db 312 gaagataatgcacactatttttgcagcagatataagttccattccacgttcgctcg 371
Qy 301 GAAGACATTGCCACTTATTTGGCAACAGGTAACACGGTTCCTCCGTACAGTTCCGAGGG 360

Db 372 gggacaaagtggaaataaa 391
Qy 361 GGGACCAAGCTGGAATAAA 380

RESULT 11
LOCUS MUSICKAVD 324 bp DNA ROD 29-OCT-1994
DEFINITION Mouse Ig rearranged kappa-chain (V-IdCR J2) gene V10-J region,
hybridoma KL2.29, partial cds.
ACCESSION M63611
KEYWORDS V-region; immunoglobulin light chain; kappa chain;
processed gene.
SOURCE Mus musculus (strain (CAL-20 x A/J) F1) B lymphocyte DNA.
ORGANISM Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (sites)
AUTHORS Sakano,H., Huppi,K., Heinrich,G. and Tonegawa,S.
TITLE Sequences at the somatic recombination sites of immunoglobulin
light-chain genes
JOURNAL Nature 280 (5720), 288-294 (1979)
MEDLINE 79221879
REFERENCE 2 (sites)
AUTHORS Wysocki,L.J., Gridley,T., Huang,S., Grandea,A.G. III. and
Geffer,M.L.
TITLE Single germline VH and V kappa genes encode predominating antibody
variable regions elicited in strain A mice by immunization with
p-azophenylarsonate
J. Exp. Med. 166 (1), 1-11 (1987)
JOURNAL 87252903
MEDLINE
REFERENCE 3 (bases 1 to 324)
AUTHORS Wysocki,L.J., Creadon,G., Lehmann,K.R. and Cambier,J.C.
TITLE B-cell proliferation initiated by Ia cross-linking and sustained by
interleukins leads to class switching but not somatic mutation in
vitro
Immunology 75 (1), 116-121 (1992)
JOURNAL 92165291
MEDLINE
COMMENT NCBI gi: 196784
FEATURES Location/Qualifiers
source 1..324
/organism="Mus musculus"
/strain=" (CAL-20 x A/J) F1"
/cell_line="hybridoma KL2.29"
/sequenced_mol="DNA"
/tissue_type="B lymphocyte"
1..>324
/gene="Igk"
/map="6"
/note="Light chain variable region of antibodies
associated with strain A response to p-azophenylarsonate;
NCBI gi: 196785"
/codon_start=1
/product="immunoglobulin kappa chain"
/translation="DIQMTQTSSLSASLGRVTISCRASQDISNYLNWYQKPDGTV
KLLIYVTSRLHSGVPSRFGSGSGTDYSLTISNLEQEDIAITYFCQQGNTLPYTFGGT
KLEIKR"
<1..>284
/gene="Igk"
/map="6"
/note="This CDS feature is included to show the

```

Jul 8 08:42

US-08-137-117B-28.rgs

16

```

V_region translation of the corresponding V_region. Presently
translation qualifiers on V_region features are illegal."
/translation="DIQMTQTSSLSASLGRVTISCRASQDISNYLNWYQKPDGTV
KLLIYVTSRLHSGVPSRFGSGSGTDYSLTISNLEQEDIAITYFCQQGNTLP"
<1..284
/gene="Igk"
/map="6"
/note="VKIdCR segment"
J_segment 285..>324
/gene="Igk"
/map="6"
/note="JK2 segment"
BASE COUNT 98 a 78 c 72 g 76 t
ORIGIN chromosome 6.
Query Match 81.4%; Score 310; DB 56; Length 324;
Best Local Similarity 98.4%; Pred. No. 0, 00e+00;
Matches 315; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 1 gatatccagatgacacagactacatcctcctgtcgtcctctctctgggacagagtcacc 60
Qy 61 GATATCCAGATGACACAGACTACATCCTCCCTGCTCCTCTCTGGGACAGAGTCACC 120
Db 61 atcagttgcaggcgaagtgcaggacatttaacattatttaactaggtatcagcagaacca 120
Qy 121 ATCAGTTGCGAGCGCAAGTCAGCAGATTAGCAGTATTATTAACTGGTATCAGCAGAAACCA 180
Db 121 gatggaactgttaactcctgatctactacatacaagattacactcaggagtcaccatca 180
Qy 181 GATGGAACTATTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
Db 181 aggttcagtgccagtggtctggaaacagattattctcaccattagcaacctggagcaa 240
Qy 241 AGGTTCAGTGGCAGTGGGCTGGAAACAGATTATTCTCTCACCATTACACCTGGAGCAA 300
Db 241 gaagataatgccacttactttgccaacagggttaactacgttccgtacacgttcggagg 300
Qy 301 GAAGACATTGCCACTTACTTTTGGCAACAGGTAACACGGTTCCTCCGTACAGTTCCGAGGG 360
Db 301 gggaccaagtggaaataaa 320
Qy 361 GGGACCAAGCTGGAATAAA 380

RESULT 12
LOCUS MMICKL229 324 bp DNA ROD 05-NOV-1994
DEFINITION M.musculus gene for immunoglobulin kappa light chain variable
region (KL2.29).
ACCESSION X55044
KEYWORDS immunoglobulin kappa light chain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; mitochondria eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chondata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 324)
AUTHORS Wysocki,L.J.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1991) to the EMBL/GenBank/DBJ databases. L.J.
Wysocki, NATIONAL JEWISH CENTER FOR IMMUNOLOGY AND RESPIRATORY
MEDICINE, DEPT OF PEDIATRICS K902, 1400 JACKSON ST, DENVER CO
80206, USA

```



```
Db 181 aggttcagtgccagtggttggaacagagattattctctcaccattagcaacacctggagcaa 240
|||||
Qy 241 AGGTTGAGTGGGAGTGGGCTGGACAGATATTCTCTACCATTAACAACCTGGAGCAA 300
|||||

Db 241 gaagatatgccacttactttggccaacaggtgaatacagcttccgtacacagtttcggagg 300
|||||
Qy 301 GAAGACATGGCCACTTACTTTGGCAACAGGTAACAGGCTTCGGTAACAGCTTCGGAGGG 360
|||||

Db 301 gggaccaagctggaataaaa 320
|||||
Qy 361 GGGACCAAGCTGGAAATAAA 380
|||||

RESULT 14
LOCUS MMIGKL233 324 bp DNA ROD 05-NOV-1994
DEFINITION M.musculus gene for immunoglobulin kappa light chain variable
region (KL2.33).
ACCESSION X55045
KEYWORDS immunoglobulin kappa light chain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonadata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 324)
Wysocki, L.J.
Direct Submission
Submitted (14-JAN-1991) to the EMBL/GenBank/DBJ databases. L.J.
Wysocki, NATIONAL JEWISH CENTER FOR IMMUNOLOGY AND RESPIRATORY
MEDICINE, DEPT OF PEDIATRICS K902, 1400 JACKSON ST, DENVER CO
80206, USA
2 (bases 1 to 324)
Wysocki, L.J., Grendon, G., Lehmann, K.R. and Cambier, J.C.
B-cell proliferation initiated by Ia cross-linking and sustained by
interleukins leads to class switching but not somatic mutation in
vitro
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 324)
Wysocki, L.J., Creadon, G., Lehmann, K.R. and Cambier, J.C.
B-cell proliferation initiated by Ia cross-linking and sustained by
interleukins leads to class switching but not somatic mutation in
vitro
JOURNAL Immunology 75 (1), 116-121 (1992)
MEDLINE 92165291
COMMENT NCBI gi: 511031
FEATURES Location/Qualifiers
source 1..324
/organism="Mus musculus"
/cell_type="B lymphocyte"
/cell_line="hybridoma; KL2.33"
/chromosome="6"
<1..>324
/note="NCBI gi: 511032"
/codon_start=1
/product="immunoglobulin kappa light chain"
/translation="DIQMGTTSLSISLGRVTISCRASQDISNLYLNWYQKPDGV
KLLIYYSRLHSVPSFSCSGSDYISLTISNLEQDIATYFCQQGNTLPTFGGCT
KLEIKR"
misc_feature 285..324
/note="Jk2 segment"
BASE COUNT 98 a 78 c 72 g 76 t
```

ORIGIN

```
Query Match 81.4%; Score 310; DB 54; Length 324;
Best Local Similarity 98.4%; Pred. No. 0.00e+00;
Matches 315; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 1 qatatcaagatcacacagactacactctcctctcgtcctcctctcgtggagacagagtcacc 60
|||||
Qy 61 CATATCCAGATCACACAGACTACATCTCCCTGTCTCTCTGGGACAGAGTCCACC 120
|||||

Db 61 atcagttgcagggaagtcaggacattagcaattatttaaaactggtatcagcagagaacca 120
|||||
Qy 121 ATCAGTTGCGAGGCAAGTCAGGACATTAGCAGTTATTAACTGCTATCAGCAGAAACCA 180
|||||

Db 121 gatggaactgtaaacctcctgatctactacatcaagattacactcaggagtcaccatca 180
|||||
Qy 181 GATGGAACATTAATAACTCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCA 240
|||||

Db 181 aggttcagtgccagtggttggaacagagattattctctcaccattagcaacacctggagcaa 240
|||||
Qy 241 AGGTTGAGTGGGAGTGGGCTGGACAGATATTCTCTCACCATTAAACCTGGAGCAA 300
|||||

Db 241 gaagatatgccacttactttggccaacaggtgaatacagcttccgtacacagtttcggagg 300
|||||
Qy 301 GAAGACATTTGCCACTTACTTTTGGCAACAGGTAACAGGCTTCGGTACAGCTTCGGAGGG 360
|||||

Db 301 gggaccaagctggaataaaa 320
|||||
Qy 361 GGGACCAAGCTGGAAATAAA 380
|||||

RESULT 15
LOCUS MUSIGKAVF 324 bp DNA ROD 29-OCT-1994
DEFINITION Mouse Ig rearranged kappa-chain (V-IdCR J2) gene V10-J region,
hybridoma KL3.8, partial cds.
ACCESSION M63613
KEYWORDS V-region; immunoglobulin light chain; kappa chain;
processed gene.
SOURCE Mus musculus (strain (CAL-20 x A/J) F1) B lymphocyte DNA.
ORGANISM Mus musculus
Eukaryotes; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (sites)
AUTHORS Sakano, H., Huppi, K., Heinrich, G. and Tonegawa, S.
TITLE Sequences at the somatic recombination sites of immunoglobulin
light-chain genes
JOURNAL Nature 280 (5720), 288-294 (1979)
MEDLINE 79221879
REFERENCE 2 (sites)
AUTHORS Wysocki, L.J., Gridley, T., Huang, S., Grandea, A.G. III. and
Geffer, M.L.
TITLE Single germline VH and V kappa genes encode predominating antibody
variable regions elicited in strain A mice by immunization with
P-azophenylarsenate
JOURNAL J. Exp. Med. 166 (1), 1-11 (1987)
MEDLINE 87252903
REFERENCE 3 (bases 1 to 324)
AUTHORS Wysocki, L.J., Creadon, G., Lehmann, K.R. and Cambier, J.C.
TITLE B-cell proliferation initiated by Ia cross-linking and sustained by
interleukins leads to class switching but not somatic mutation in
vitro
JOURNAL Immunology 75 (1), 116-121 (1992)
MEDLINE 92165291
COMMENT NCBI gi: 196788
```

Jul 8 08:42

US-08-137-117B-28.fgc

21

FEATURES
source Location/Qualifiers
1..324
/organism="Mus musculus"
/strain="CAL-20 x A/J) F1"
/cell_line="hybridoma KL3.8"
/sequenced_mol="DNA"
/tissue_type="B lymphocyte"
<1..>324
/gene="Igk"
/map="6"
/note="light chain variable region of antibodies associated with strain A response to p-azophenylarsonate; NCBI gi: 196789"
/codon_start=1
/product="immunoglobulin kappa chain"
/translation="DIQMTQTTSLSASLGDRVTISCRASQDISINLYNWYQKQPDGTV
KLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIAITYFCQQGNTLPYTFGGGT
KLEIKR"
<1..>284
/gene="Igk"
/map="6"
/note="This CDS feature is included to show the translation of the corresponding V region. Presently translation qualifiers on V_region features are illegal."
/translation="DIQMTQTTSLSASLGDRVTISCRASQDISINLYNWYQKQPDGTV
KLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIAITYFCQQGNTLP"
<1..284
/gene="Igk"
/map="6"
/note="VKIdCR segment"
285..>324
/gene="Igk"
/map="6"
/note="JK2 segment"
BASE COUNT 98 a 78 c 72 g 76 t
ORIGIN chromosome 6.

Query Match 81.4%; Score 310; DB 56; Length 324;
Best Local Similarity 98.4%; Pred. No. 0.00e+00;
Matches 315; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 1 gatattccagatgacacagctacatctccctgtctgctctctctgtggagacagagtcacc 60
QY 61 GATATCCAGATGACACAGCTACATCCTCCTGCTGCTCTGCGCTCTCTGGGAGACAGAGTCACC 120
Db 61 atcagttgcaggcgaagtgcagcattagcaattatttaaacgtgtatcagcagaaacca 120
QY 121 ATCAGTTGCAGGCGCAAGTCAGGACATTAGCAGTTATTAAACTGGTATCAGCAGAAACCA 180
Db 121 gatggaactgttaaactcctgactactacacatacaagattacactcaggaggtcccatca 180
QY 181 GATGGAACATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCA 240
Db 181 aggttcagtggcagtggtgtcgaacagattattctcaccattagcaacctggagcaa 240
QY 241 AGGTTTCAGTCGCGAGTGGGTCTGGACAGAGATTATTCTCTCACCATTAACAACTGGAGCAA 300
Db 241 gaagatattgccacttacttttgccaacagggtaatacgtctccgtacacgttcggaggg 300
QY 301 GAAGACATTGGCACTTACTTTTGGCAACAGGGTACACGCTTCGGTACACGTTGGAGGG 360
Db 301 gggacacaagctggaaataaa 320
QY 361 GGCACCAAGCTGGAATAAA 380

Jul 8 08:42

US-08-137-117B-28.fgc

22

Search completed: Mon Jul 8 08:52:40 1996
Job time : 271 secs.

WATERMAN

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:52:57 1996; MacPar time 33.66 Seconds
752.688 Million cell updates/sec

Tabular output not generated.

Title: >US-08-137-117B-28

Description: (1-381) from US08137117B.seq

Perfect Score: 381

N.A. Sequence: 1 ATGGTCTCTCAGCTCAGCT.....GGACCAAGCTGGAATAAAT 381

Comp: TACCACAGGAGTCTGACTCAA.....CTGGTTCGACCTTTATTTA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 84802 seqs, 33246950 bases x 2

Post-processing: Minimum Match 0\$
Listing first 45 summaries

Database: n-geneeq22

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 8.229; Variance 4.974; scale 1.655

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	381	100.0	381	5 Q30755	pPM-k3.	2.64e-243
2	354	92.9	381	6 Q36607	Anti-CD4 antibody MT	2.63e-224
3	354	92.9	393	16 T05311	MAB SCH94.03 light ch	2.63e-224
4	344	90.3	381	7 Q45662	Mouse C4G1 Ig light-c	2.82e-217
5	340	89.2	444	5 Q08608	ME4 Light Chain V Reg	1.82e-214
6	334	87.7	381	5 Q30759	pl46-k3.	2.98e-210
7	323	84.8	372	10 Q56067	Human IL-1 chimeric a	1.57e-202
8	322	84.5	402	2 Q12017	Sequence encoding mou	7.88e-202
9	322	84.5	402	2 Q12061	Sequence encoding lig	7.88e-202

10	304	79.8	408	6 Q37058	Rat immunoglobulin L	3.28e-189
11	304	79.8	408	11 Q45438	RW641 H chain variabl	3.28e-189
12	294	77.2	324	16 T05313	B-cell lymphoma CH12	3.30e-182
13	280	73.5	913	12 Q81076	Bispecific CD3-L6Fvlg	2.05e-172
14	275	72.2	831	10 Q62957	Anti-Influenza N10 sc	6.41e-169
15	244	64.0	627	13 Q80294	Monoclonal antibody 1	2.68e-147
16	208	54.6	389	14 Q67194	Humanized 1308F VL DN	2.66e-122
17	206	54.1	450	4 N30165	Sequence encoding the	6.44e-121
18	198	52.0	400	7 Q44069	H65 light chain varia	2.19e-115
19	196	51.4	388	6 Q34574	Plasmid pXOM2.	5.28e-114
20	192	50.4	321	16 Q97504	Light chain variable	3.05e-111
21	192	50.4	321	16 Q97507	Light chain variable	3.05e-111
22	192	50.4	321	16 Q97510	Light chain variable	3.05e-111
23	189	49.6	419	1 Q05556	Sequence encoding var	3.58e-109
24	188	49.3	449	13 Q78732	Murine anti-human ath	1.75e-108
25	187	49.1	739	8 Q46084	Sequence encoding 520	8.58e-108
26	184	48.3	390	15 Q87237	Anti-interleukin-1 al	1.00e-105
27	179	47.0	1605	8 Q46086	Sequence encoding G-F	2.77e-102
28	178	46.7	387	14 Q82749	93K9 anti-Varicella	1.35e-101
29	177	46.5	618	2 Q11191	V region gene JP2qL41	6.59e-101
30	177	46.5	618	2 Q10946	Feline immunoglobulin	6.59e-101
31	177	46.5	702	7 Q43773	Sequence encoding the	6.59e-101
32	176	46.2	384	11 Q64056	Sequence of the VL re	3.21e-100
33	176	46.2	402	11 Q45430	KM-603 light chain.	3.21e-100
34	174	45.7	1066	8 Q49943	Human anti-HBs light	7.61e-99
35	173	45.4	467	2 Q12631	Murine OKT4A light ch	3.70e-98
36	173	45.4	599	13 Q73537	ME1-14 light chain va	3.70e-98
37	173	45.4	723	7 Q42285	V-J(gamma)/((Gly)4Ser	3.70e-98
38	172	45.1	321	13 Q75546	Humanised antibody he	1.80e-97
39	172	45.1	321	7 Q42268	Encodes kappa chain V	1.80e-97
40	172	45.1	381	6 Q36611	Anti-IL2R-alpha antib	1.80e-97
41	172	45.1	432	3 Q15113	IL-2 chimeric antibod	1.80e-97
42	172	45.1	432	3 Q15114	IL-2 chimeric antibod	1.80e-97
43	171	44.9	645	14 Q67895	cDNA contg. an ORF fo	8.75e-97
44	171	44.9	945	3 Q20067	Encodes light chain o	8.75e-97
45	170	44.6	723	7 Q42284	V-J(kappa)/((Gly)4Ser	4.25e-96

ALIGNMENTS

RESULT	1
ID	Q30755 standard; cDNA; 381 BP.
AC	Q30755;
DT	30-MAR-1993 (first entry)
DE	pPM-k3.
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; PM1;
KW	plasmid; pPM-k3; pPM-H1; ss.
OS	Synthetic.
FT	Key Location/Qualifiers
FT	sig_peptide 1..60
FT	/*tag= a
FT	mat_peptide 61..381
FT	/*tag= b
PN	WO9219759-A.
PD	12-NOV-1992.
PF	24-APR-1992; J00544.
PR	25-APR-1991; JP-095476.
PR	19-FEB-1992; JP-032084.
PA	(CHUS) CHUGAI SEIYAKU KK.
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR	WPI; 92-398882/48.
DR	P-PSDB; R28670.
PT	Reconstituted human antibody to human interleukin-6 receptor -

DT	04-MAR-1993 (first entry)	
DE	ME4 Light Chain V Region (mouse).	
KW	Monoclonal antibody; chimera; light; heavy; chain; constant;	
KW	variable; antigen; diagnosis; cancer; tumour; ss.	
FS	Mus musculus.	
OH		
FT	Key	Location/Qualifiers
FT	CDS	61..444
FT	/*tag= a	
FN	W09002569-A.	
PD	22-MAR-1990.	
PF	06-SEP-1989; U03852.	
PR	06-SEP-1988; U034624.	
PR	08-SEP-1988; U0341744.	
PR	13-SEP-1988; U0243739.	
PR	04-OCT-1988; U0253002.	
PR	19-JUN-1989; U0367641.	
PR	21-JUL-1989; U0382768.	
PA	(ITGE-) INT GENETIC ENG INC.	
PA	Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;	
DR	WPI; 90-115825/15.	
DR	P-PSDB; R09426.	
PT	Chimeric mouse-human antibodies - prep'd. using genes coding for	
PT	constant human region murine variable region, esp. to 3 tumour	
PS	antigen	
PS	Claim 13; Page 123 + Fig 29; 173pp; English.	
CC	Shown is the nucleotide sequence from the end of the oligo-dC tail	
CC	to the Jk1-Ck junction. The sequence is used in the prodn. of a	
CC	chimeric antibody mol. comprising two light chains and two heavy chains,	
CC	each having a constant region (human) and a variable region (murine)	
CC	having specificity to an antigen bound by murine monoclonal antibody	
CC	(WAB) ME4. The chimeric antibodies can be used for any purpose for	
CC	which the original murine MAbs can be used, with the advantage that	
CC	they are more compatible with the human body. They are esp. used for	
CC	the diagnosis and treatment of cancer.	
SQ	Sequence 444 BP; 109 A; 122 C; 94 G; 119 T;	
Query Match	89.2%; Score 340; DB 5; Length 444;	
Best Local Similarity	94.7%; Pred. No. 1.82e-214;	
Matches	360; Conservative 0; Mismatches 20; Indels 0; Gaps 0;	

Db	61	atgatgctctctgctcagttcccttgggtctcctgtgtctcctgtgtctgttttcaaggtaccagatgt	120
Qy	1	ATGGTGCTCTCAGCTCAGTTCCTTGGTCTCCTGTGCTGCTCTGTTTTCAAGTACCAGATGT	60
Db	121	gataccagatgacacagactacatcctctgctgcctctctgggagacagagtcaacc	180
Qy	61	GATATCCAGATGACACAGACTACATCCTCCCTGTGCTCTCTGGGACAGACAGTCAACC	120
Db	181	atcagttgcagggcgaagtcagagcattaccacttattaaactgggtatcagcagaagacca	240
Qy	121	ATCAGTTGCAGGCGAAGTCAGACATTTACAGTTATTTTAACTGGTATCAGCAGAAACCA	180
Db	241	gatggaactgftaaactcctgatctactacatcaagattacactcagaggtcccatca	300
Qy	181	GATGGAACTATTTAAACTCCTGATCTACTACATCAGATATTAACCTCAGGAGTCCCATCA	240
Db	301	aggttcadgtgcagtggtctggaacagattatctctcaccattagcaacctggaqcaa	360
Qy	241	AGGTTCACTGGCAGTGGGTCTGGAACAGATTATTTCTCACCATTAAACAACCTTGGAGCAA	300
Db	361	gaagattttgccacttacttttgccaacagggttaataactctcctcggaagttcagtgga	420
Qy	301	CAGACATTTGCCACTTATCTTTTGGCCACAGGGTAAACAGCTTCGTACAGTTTCGGAGGG	360

Db	421	ggaccacaaactgggaatcaa	440
Qy	361	GGGACCAAGCTGGAAATAA	380
RESULT	6		
ID	Q30759	standard; cDNA; 381 BP.	
AC	Q30759;		
DT	30-MAR-1993	(first entry)	
DE	p146-k3.		
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;		
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;		
KW	plasmid; p146k3; p146-h1; ss.		
OS	Synthetic.		
Key	Key	Location/Qualifiers	
FT	sig_peptide	1..60	
FT	/*tag= a		
FT	mat_peptide	61..381	
FT	/*tag= b		
PN	W09219759-A.		
PD	12-NOV-1992.		
PF	24-APR-1992; J00544.		
PF	25-APR-1991; JP-095476.		
PR	19-FEB-1992; JP-032084.		
PA	(CHUS) CHUGAI SEIYAKU KK.		
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;		
DR	WPI; 92-398892/48.		
DR	P-PSDB; R29010.		
PT	Reconstituted human antibody to human interleukin-6 receptor -		
PT	has low antigenicity and contains mouse V-region complementarity		
PT	determining regions		
PS	Disclosure; Page 127-128; 207pp; Japanese.		
CC	The sequences given in Q30759 and Q31337 were used in example to		
CC	illustrate the production of a human antibody which recognises human		
CC	interleukin-6 receptor (IL-6R). The antibody comprises light (L)		
CC	chain and heavy (H) chain variable regions which were derived from a		
CC	mouse monoclonal antibody produced from the hybridoma AUK146-15 which		
CC	contained the plasmids p146-k3 and p146-h1.		
SQ	Sequence 381 BP; 106 A; 90 C; 86 G; 99 T;		

Query Match	87.7%;	Score 334;	DB 5;	Length 381;
Best local Similarity	93.9%;	Pred. No. 2,98e-210;		
Matches 357;	Conservative	0;	Mismatches 23;	Indels 0; Gaps 0;
Db	1	atggtgtccacacctcagttccttgggtctctctggtgatctgttttcaaggtaccagatgt	60	
Qy	1	ATGGTGTCTCAGCTCAGTTCCTTGGTCTCCTGTGCTCTGTGTTTCAGGTACCAGATGT	60	
Db	61	gatatccagatgacacagactacatcctccctgtctgcctctctgggagacagagtccacc	120	
Qy	61	GATATCCAGTGAACACAGACTAGATCCTCCCTGTCTGCCTCTCTCGGAGACAGAGTCACC	120	
Db	121	atcagttgcaggcgaagtccaggacattagtaattattaaactgggtatcaacagaagaacca	180	
Qy	121	ATCAGTTGCGAGGCGAAGTCAGAGCAITTAGCAGCTATTATTAACCTGGTATCAGCAAGAACA	180	
Db	181	gatggaaactggtaaactcctgatctacgatatacaagattacactcagaggtcccatca	240	
Qy	181	GATGGAAACTTTTAAACTTCCTGATCTACTACATCAAGATTACACTAGAGAGTCCCATCA	240	
Db	241	aggttcagtggcactgggtctcggaacagattatctctcaaccattagcaacctggagcaa	300	
Qy	241	AGGTTTCAGTGGCAGTGGGTCTGGAAAGATTATTTCTCTACCAATTAACAACCTTGGAGCAA	300	

Db	301	gaagatattgcagttactatttgccaaacagggtataacgcctcctggacggttcggtgga	360
Qy	301	GAAGACAATGCCACTTACTTTTTCACACAGGGTAACAGCTTCCGTTACAGTTCGGAGGG	360
Db	361	ggcaccagaattggaaatacaa	380
Ov	361	GGGACCAAGCTGGAAATAAA	380

RESULT 7

ID	Q56067	standard; cDNA to mRNA; 372 BP.
AC	Q56067;	
DT	09-AUG-1994	(first entry)
DE	Human IL-1 chimeric antibody CH cDNA.	
PR	Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;	
KW	light; L; chain; constant; region; variable; mouse; anti-human;	
KW	graft; CDR; complementarity determining region; heavy; H;	
KW	inflammatory disease; arteriosclerosis; detection;	
KW	diffused intravascular coagulation; leukemia; ss.	
OS	Synthetic.	
EH	Key	Location/Qualifiers
FT	sig_peptide	1..93
FT	/*tag= a	
FT	mat_peptide	94..372
FT	/*tag= b	
PN	W09402627-A.	
PD	03-FEB-1994.	
PP	08-JUL-1993; J00941.	
PR	16-JUL-1992; JP-189248.	
SA	(SAKA) OTSUKA PHARM CO LTD.	
PI	Hirai Y, Nishida T, Omoto Y, Owens RJ;	
DR	WFI; 94-048885/06.	
DR	P-PSDB; R47206.	
PT	Mouse/human chimeric antibody against human interleukin-1 - for	
PT	treatment of diseases in which production of interleukin-1 is	
PT	abnormal, and for diagnostic imaging of interleukin-1 production	
PT	sites in vivo	
PS	Claim 1; Page 31-32; 58pp; Japanese.	
CC	The sequences given in Q56066-69 are the coding sequences for the	
CC	light and heavy chain, variable and constant regions of a chimeric	
CC	recombinant antibody against human interleukin-1 (IL-1). The antibody	
CC	has a light (L) chain in which the constant region is that of a human	
CC	antibody and the variable region is from a mouse anti-human IL-1	
CC	antibody or is a mouse-human graft containing the CDR regions of mouse	
CC	anti-human IL-1 antibody, and a heavy (H) chain in which the constant	
CC	region is that of a human antibody and the variable region is from a	
CC	mouse anti-human IL-1 antibody or is a mouse-human graft containing	
CC	the CDR regions of mouse anti-human IL-1 antibody, . The chimeric	
CC	antibody is used to treat diseases in which abnormal amounts of IL-1	
CC	are produced, eg. inflammatory disease, arteriosclerosis, diffused	
CC	intravascular coagulation or leukemia. It can also be labelled and	
CC	used for diagnostic imaging of IL-1 producing sites in vivo.	
SQ	Sequence 372 BP; 105 A; 93 C; 78 G; 96 T;	

Query Match 84.8%; Score 323; DB 10; Length 372;
Best Local Similarity 93.5%; Pred. No. 1.57e-202;
Matches 347; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy	70	ATGACACAGACTACATCCCTCCCTGCTCGCTCTCTGGGAGACAGATCCACCATCAGTTGC	129
Db	121	aggcaagt-cagacattacaataaattaaactggtttcaacagaacacagatggaaact	180
Qy	130	AGGGCAACTCAGGACATTAGCAGTTATTTAAACTGGTATCAGCAGAAACCATGGAACT	189
Db	181	gttaaaactcctgatatcaatcacatcaagattacaactcaggagtcacctcaagattcagtt	240
Qy	190	ATTTAAACTCCTGATCTACTACATCAAGATTACACTCAGGAGTCCCATCAAGTTCAGT	249
Db	241	ggcagtggtgtctggaacagattattctcaccattagcaacctggaaagaagaatgct	300
Qy	250	GGCAGTGGGTCTGGACACATTATTTCTCCACATTAAACAACCTGGAGCAAGACGACATT	309
Db	301	gccacttacttttgccaacacaggttaaaaccccttcctgtggacgttcggtggagggcaaccaag	360
Qy	310	GCCACTTACTTTTGGCAACAGGGTAAACGGTTCCTCGGTACACGTCGGGAGGGGGGACCAAG	369
Db	361	ctggaattcaa	371
Qy	370	CTGCAAAATAAA	380

RESULT

ID	Q12017 standard; DNA; 402 BP.
AC	Q12017;
DT	19-AUG-1991 (first entry)
DE	Sequence encoding mouse MAb 1C11 L chain V region.
KW	HIV-1; chimera; ds.
OS	Mus sp.
FH	Key
FT	CD5
FT	Location/Qualifiers
FT	22..402
FT	/*tag= a
PN	W09107494-A.
PD	30-MAY-1991.
PF	13-NOV-1990; U06627.
PR	13-NOV-1989; US-433703.
PA	(XOMA-) Xoma Corp.
PI	Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
DR	WPI; 91-178106/24.
DR	P-PSDB: R12237.

PT New chimeric mouse human antibodies - used in treatment, diagnosis
PT and prophylaxis of HIV infections.
PS Disclosure; Fig 13; 108pp; English.
CC The mouse VL gene product may be used to produce chimeric mouse-
CC human Abs against HIV-1 comprising human Ig constant regions and
CC murine variable regions. These novel sequence are useful in
CC treatment, diagnosis and prophylaxis of HIV infections, and may be
CC produced by a bacterial, yeast or mammalian expression system.
SQ Sequence 402 BP; 108 A; 99 C; 88 G; 107 T;

Query Match 84.5%; Score 322; DB 2; Length 402;
Best Local Similarity 92.4%; Pred. No. 7.88e-202;
Matches 351; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db	22	atgatgctctgctcagttcccttggtctctctgttgctctgtttccaaggtaccagatgt	81
Qy	1	ATGGTGTCTCAGCTCAGTTCCTTGGTCTCCTGTGCTGCTTTTCAAGTACCA	60
Db	82	gatatccagatgacacagactacatcctccctgtctgcctctctggagacagagtccacc	141
Qy	61	GATATCCAGATGACACAGACTACATCCTCCCTGTGCTGCTCTGGGAGACAGAGTACC	120
Db	142	atcagttgcagttgcagagtcaggcgattacgaattattttaaacattgatatcagcaga	201

PR	28-MAY-1993; US-070160.
PA	(SCRI) SCRIPPS RES INST.
PI	Leturcq DJ, Mathison JC, Moriarty AM, Tobias PS;
PI	Ulevitch RJ;
DR	WPI; 95-022719/03.
DR	p-PsDB; R64204.
PT	Hybridoma cell lines produce MAb which inhibit CD14-mediated cell
PT	activation - for detecting CD14 in a sample and to inhibit the
PT	binding of LPS to CD14.
PS	Disclosure; Fig 5; 91pp; English.
CC	Anti-human soluble CD14 receptor MAB 18E12 may be used to
CC	detect CD14 in cell samples, to inhibit binding of LPS to
CC	CD14 or a LPS/CD14 complex to a cell, to inhibit CD14-mediated
CC	activation of a cell expressing CD14 receptor, and for sepsis
CC	therapy.
SQ	Sequence 627 BP; 184 A; 161 G; 139 T;
	Query Match 64.0%; Score 244; DB 13; Length 627;
	Best Local Similarity 91.6%; Pred. No. 2.68e-147;
	Matches 285; Conservative 0; Mismatches 23; Indels 3; Gaps 1;

Db	61	aggcgcaagtccaggacattaaagaattattttaaacctggtatctcaagcaggagaccgaagtggaaact	120
Qy	130	AGGCGCAAGTCAGGACATTAGCAGCTATTTTAAACTGGTATTCAGCAGCAAAACCGAGATGGAAT	189
Db	121	gttaaggtccctaatctactacacatcaagattacaactccaggaggtcccatccaaggttcaggt	180
Qy	190	ATTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAGTCCCATCAAGGTTCCAGT	249
Db	181	ggcagtggtgtctggacaagattattctctcaaccattagacaacctggagacaagaagaattttt	240
Qy	250	GGCAGTGGGCTGGAAACAGATTATTCCTCACCAATTAAACAACCTGGAGCAAGAAGACATT	309
Db	241	gcaacttaacttt---caacgggggtgatacggttcctggacacttcggtggagggacacaag	297
Qy	310	GCCACTTACTTTTCCCAACAGGGGTACAGCGCTCCGTACACGCTTCGGAGGGGGGCCAACG	369
Db	298	ctggaaatcaa	308
Ov	370	CTGGAAATAA	380

Search completed: Mon Jul 8 08:53:37 1996
Job time : 40 secs.

RESULT	15
ID	Q80294 standard; DNA; 627 BP.
AC	Q80294;
DT	08-JUL-1995 (first entry)
DE	Monoclonal antibody 18E12 light chain.
KW	CD14 receptor; monoclonal antibody; 18E12; hybridoma;
KW	antiseptic; therapeutic; ds.
OS	Homo sapiens.
FH	Key
	Location/Qualifiers
FT	mat_peptide
FT	1..627
FT	/*tag= a
PN	W09428025-A.
PD	08-DEC-1994.
PF	27-MAY-1994; U05898.

TVAQSPRLA (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MParch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:53:55 1996; MacPar time 178.28 Seconds

Tabular output not generated.
768.287 Million cell updates/sec

Title: >US-08-137-117B-28

Description: (1-381) from US081371117B.seq

Perfect Score: 381

N.A. Sequence: 1 ATGGTCTCTCAGTCAGCT.....GGACCAAGTCGGAATAAAT 381

Comp: TACACAGAGTCAGTCA.....CCTGGTCAGCTTTATTTA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-STS

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94
EST-STS-TWO
95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5
100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10
105:gnEST11 106:gnEST12 107:gnEST13 108:gnEST14 109:gnEST15
110:gnEST16 111:gnEST17 112:gnEST18 113:gnEST19 114:gnEST20
115:gnEST21 116:gnEST22 117:gnEST23 118:gnEST24 119:gnEST25
120:gnEST26 121:gnEST27 122:gnEST28 123:gnEST29
124:gnEST30 125:gnEST31 126:gnEST32 127:gnEST33

Database:

95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5
100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10
105:gnEST11 106:gnEST12 107:gnEST13 108:gnEST14 109:gnEST15
110:gnEST16 111:gnEST17 112:gnEST18 113:gnEST19 114:gnEST20
115:gnEST21 116:gnEST22 117:gnEST23 118:gnEST24 119:gnEST25
120:gnEST26 121:gnEST27 122:gnEST28 123:gnEST29
124:gnEST30 125:gnEST31 126:gnEST32 127:gnEST33

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

Statistics: Mean 10.019; Variance 1.775; scale 5.646

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	178	46.7	393	69	T27593	EST100653 Homo sapien	0.00e+00
2	178	46.7	393	127	HST27593	EST100653 Homo sapien	0.00e+00
3	176	46.2	516	52	R67559	y142h11.r1 Homo sapie	0.00e+00
4	165	43.3	395	114	HS11211	EST69384 Homo sapiens	0.00e+00
5	165	43.3	395	70	T29112	EST69384 Homo sapiens	0.00e+00
6	146	38.3	288	69	T27581	EST100107 Homo sapien	9.92e-265
7	146	38.3	288	127	HST27581	EST100107 Homo sapien	9.92e-265
8	138	36.2	288	69	T27721	EST13641 Homo sapiens	1.80e-246
9	138	36.2	288	127	HST27721	EST13641 Homo sapiens	1.80e-246
10	124	32.5	451	42	R31204	yh62a07.r1 Homo sapie	1.01e-214
11	120	31.5	335	47	R49881	yj55f09.r1 Homo sapie	1.05e-205
12	115	30.2	243	11	H25952	y156a07.r1 Homo sapie	1.81e-194
13	108	28.3	503	41	R28232	yh57e08.r1 Homo sapie	8.10e-179
14	107	28.1	463	53	R69532	yj82d09.r1 Homo sapie	1.37e-176
15	100	26.2	332	118	HS34210	EST77181 Homo sapiens	4.69e-161
16	100	26.2	332	70	T29342	EST77181 Homo sapiens	4.69e-161
17	93	24.4	279	122	HS65610	EST89211 Homo sapiens	1.22e-145
18	93	24.4	279	70	T29656	EST89211 Homo sapiens	1.22e-145
19	90	23.6	451	86	T90236	ye15d10.r1 Homo sapie	4.50e-139
20	85	22.3	434	87	T93178	ye24e07.r1 Homo sapie	3.45e-128
21	84	22.0	210	53	R69482	yj83c03.r1 Homo sapie	5.06e-126
22	82	21.5	360	56	R79907	y185f01.r1 Homo sapie	1.07e-121
23	79	20.7	383	70	T29916	EST99871 Homo sapiens	3.07e-115
24	79	20.7	383	125	HS91615	EST99871 Homo sapiens	3.07e-115
25	78	20.5	397	47	R49771	yj55c03.r1 Homo sapie	4.29e-113
26	77	20.2	261	46	R46878	yj54h03.r1 Homo sapie	5.94e-111
27	76	19.9	381	114	HS11411	EST69430 Homo sapiens	8.15e-109
28	76	19.9	381	70	T29114	EST69430 Homo sapiens	8.15e-109
29	72	18.9	166	11	H25744	y150a11.r1 Homo sapie	2.62e-100
30	71	18.6	385	11	H26475	y151e05.r1 Homo sapie	3.42e-98
31	70	18.4	122	10	H21703	y129d03.r1 Homo sapie	4.41e-96
32	69	18.1	390	17	H45841	yp22b04.r1 Homo sapie	5.63e-94
33	69	18.1	390	124	HS841242	yp22b04.r1 Homo sapie	5.63e-94
34	68	17.8	438	51	R64693	y122f09.r1 Homo sapie	7.10e-92
35	67	17.6	383	69	T27870	EST19007 Homo sapiens	8.84e-90
36	67	17.6	383	127	HST27870	EST19007 Homo sapiens	8.84e-90
37	66	17.3	218	12	H27031	y165d01.r1 Homo sapie	1.09e-87
38	64	16.8	213	11	H25521	y147d10.r1 Homo sapie	1.59e-83
39	64	16.8	387	53	R70292	yj81e03.r1 Homo sapie	1.59e-83
40	63	16.5	123	115	HS154207	yq66g05.r1 Homo sapie	1.88e-81
41	63	16.5	123	61	R98154	yq66g05.r1 Homo sapie	1.88e-81
42	59	15.5	133	11	H24601	y140b02.r1 Homo sapie	3.19e-73
43	59	15.5	189	57	R83213	yp11d10.r1 Homo sapie	3.19e-73
44	59	15.5	359	12	H27642	y161g07.r1 Homo sapie	3.19e-73
45	59	15.5	488	11	H25625	y148g05.r1 Homo sapie	3.19e-73

ALIGNMENTS

RESULT	1	T27593	393 bp	mRNA	EST	06-SEP-1995
LOCUS						

RA	White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
RA	Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
RA	FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geohagen N.S.M.,
RA	Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,
RA	Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,
RA	Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
RA	Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
RA	Sauadek D.W., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
RA	Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
RA	Coleman T.A., Collins E.J., Dinke D., Feng P., Ferrie A.,
RA	Fischer C., Hastings G.A., He W.W., Hu J.J.S., Greene J.M.,
RA	Gruber J., Hudson P., Kim A., Korzak D.L., Kunsch C., Ji H., Li H.,
RA	Melissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,
RA	Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rozen C.A.,
RA	Hasetline W.A., Fields C., Fraser C.M., Venter J.C.;
RT	*Initial Assessment of Human Gene Diversity and Expression
RT	Patterns Based Upon 52 Million Basepairs of cDNA Sequence";
RL	Unpublished.
CC	Other ESTs: THC24356 Contact: Venter, JC The Institute for Genomic
CC	Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056
CC	CC Fax: 3018699423 Email: tdbinfo@tigr.org For clone availability,
CC	additional sequence and expression information related to this EST,
CC	please contact the TIGR Database (tdbinfo@tigr.org). NCBI gi:
CC	609819
FE	Key Location/Qualifiers
FT	source 1..288
FT	/organism="Homo sapiens"
FT	/note="human"
FT	mRNA <1..>288
FS	Sequence 288 BP; 65 A; 75 C; 70 G; 67 T; 11 other;
Query Match	36.2%; Score 138; DB 127; Length 288;
Best Local Similarity	76.2%; Pred. No. 1.80e-246;
Matches	214; Conservative 0; Mismatches 63; Indels 4; Gaps
Db	5 gtcagctccctggggtcctnctactntggctccaggagtgcacagatgaacatccagatg 64
Qy	
13	GCTCAGTTCCTGGTGCTCTGTCTGTTTCAAGGTACAGATGTGATATCCAGATG 72
Db	65 acccagttccatcgctccctgtngcatcntnaggacagagtcaccatcaccttgccgg 124
Qy	
73	ACACAGACTACATCTCCCTGTCTGCTCTCTGGGACACAGAGTCACCATCGATTGGAGG 132
Db	125 gcaagtnagagcatagcagctatttaanttgttatcagcagaacaacaggaaagccccct 184
Qy	
133	GCAAGTCAGGACATTAGCAGTTATTTTAAACTGGTATCAGCAGAACACAGATGGAATACT 192
Db	185 aaagctcctnatctatgctgatccagctttgcaaaagtggggggtcccatacaggttcagtg 244
Qy	
193	AAACTCCTCATCTACTACATCAAGAATTACACTCAGGAG-TCCCATCAAGGTTCAAGTGG 251
Db	245 gcagtgagatctggggacagattnnanttnaccatcagea 285
Qy	
252	-CAGTGGG-TCTGGA-ACAGATTATTCTCTCCACCAATAACA 289
RESULT	10
LOCUS	R31204 451 bp mRNA EST 28-APR-1995
DEFINITION	yh6za07.r1 Homo sapiens cDNA clone 134292 5' similar to
	gb:X00965_cds1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN);
ACCESSION	R31204
KEYWORDS	EST.
SOURCE	human clones=134292 library=Soares placenta Nb2HP vector=pT7D3D

<p>(Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M3R1 Rstlet=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAGATTCGGCGCCGAGGAATTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.</p>	<p>ORGANISM</p> <p>Homo sapiens</p>
<p>REFERENCE</p> <p>AUTHORS</p>	<p>Eucauyotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.</p> <p>1 (bases 1 to 451)</p> <p>Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Narra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.</p>
<p>TITLE</p> <p>JOURNAL</p> <p>COMMENT</p>	<p>The WashU-Merck EST Project</p> <p>Unpublished (1995)</p> <p>Contact: Wilson RK</p> <p>WashU-Merck EST Project</p> <p>Washington University School of Medicine</p> <p>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108</p> <p>Tel: 314 286 1800</p> <p>Fax: 314 286 1810</p> <p>Email: est@watson.wustl.edu</p> <p>High quality sequence stops: 218</p> <p>Source: IMAGE Consortium, LNL</p> <p>This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.</p>

```

NCBI gi: 787047
FEATURES             source
    Location/Qualifiers
        1..451
            /organism="Homo sapiens"
            /clone="134292"
            /note="human"
BASE COUNT          99 a 110 c 117 g 116 t 9 others
ORIGIN
Query Match          32.5%; Score 124; DB 42; Length 451;
Best Local Similarity 82.6%; Pred. No. 1.01e-214;
Matches 161; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

Db 46 gctcagctctggggctctgctactctggtccgaggtgccagatgtgacatccagatg 105
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 13 gctcagttccttggtctcctgtgctctgttttcaaggtaccagatgtgatattccagatg 72

Db 106 accagttctccatctcctctgctgcgactgtgaggagacagatgccatcccttgcgcg 165
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 73 ACACAGACTACATCTCCCTGTCCTGTCCTCTCTGGAGACAGATGCCATCAGTTGCAGG 132

Db 166 gcaagtcagaccattagcgaactatttaaatggatcagcagaacaccagngaaagcccc 225
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 133 GCAAGTCAGGACATTAGCAGTATTTTAAACTGTATCAGCAGAAACCGAGTGGAA-CTAT 191

Db 226 taaactnctgatcta 240
      ||||| ||||| |||||
Qy 192 TAAACTCCTGATCTA 206

RESULT 11

```

Jul 8 08:46

US-08-137-117B-28.rst

15

LOCUS R49881 335 bp mRNA EST 18-MAY-1995
DEFINITION YJ55f09.r1 Homo sapiens cDNA clone 152681 5' similar to
gb:X00965_cds1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN); .
ACCESSION R49881
KEYWORDS EST.
SOURCE human clone=152681 library=Soares breast 2NbhBst vector=pf7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13P1 Reitel=Not I Reite2=Eco RI Adult female.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTCAAGTCGAGCGCGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pfT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 230. Library constructed by Bento
Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 335)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 235
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 811783
Location/Qualifiers
source 1..335
/organism="Homo sapiens"
/clone="152681"
/note="human"

BASE COUNT 74 a 92 c 83 g 85 t 1 others
ORIGIN

Query Match 31.5%; Score 120; DB 47; Length 335;
Best Local Similarity 78.0%; Pred. No. 1.05e-205;
Matches 195; Conservative 0; Mismatches 51; Indels 4; Gaps 4;

Db 23 gtcagctctggggtcctgctactctggctccaggtgccagatgtgacatccagatg 82
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 13 GCTCAGTTCCTTGGTCTCTGCTGCTGCTTTCAGGTACGAGTGCATATCAGATG 72
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 accagctctccatcttccctgtctgtctgttaggagacagatcaccatcacttgcgg 142
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 73 ACACAGACTACATCCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 gcaatcagacatcaacaactcttaatttgatcagcaaaaaccaggaggaccccc 202
||||| ||||| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||

Jul 8 08:46

US-08-137-117B-28.rst

16

Qy 133 GCAAGTCAGACATTAGCAGTTATTTAATCTGCTATCATCAGCAAAACAGATG-GAAGTAT 191
Db 203 tcaagctcctgatctcttcatcctaatttgcgaagtgggggtcccatctagggtcagt 262
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 192 TAAACTCTCTGATCTACTACATCAATACATCTAGCTAGGAG-TCCCATCAAGG-TTCAGT 249
Db 263 ggcagctggg 272
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 250 GG-CAGTGGG 258

RESULT 12
LOCUS HZ5952 243 bp mRNA EST 10-JUL-1995
DEFINITION v15fa07.r1 Homo sapiens cDNA clone 162228 5' similar to
gb:X00965_cds1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN); .
ACCESSION HZ5952
KEYWORDS EST.
SOURCE human clone=162228 library=Soares breast 3NbhBst vector=pf7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13P1 Reitel=Not I Reite2=Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTCAAGTCGAGCGCGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pfT73 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 243)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 895075
Location/Qualifiers
source 1..243
/organism="Homo sapiens"
/clone="162228"
/note="human"

BASE COUNT 52 a 73 c 65 g 51 t 2 others
ORIGIN

Query Match 30.2%; Score 115; DB 11; Length 243;
Best Local Similarity 79.3%; Pred. No. 1.81e-194;
Matches 153; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Email: estevatson.wustl.edu
 High quality sequence stops: 394
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

```
NCBI gi: 843049
FEATURES
Location/Qualifiers
1..463
/organism="Homo sapiens"
/clone="155249"
/note="human"
```

BASE COUNT	103 a	125 c	115 g	114 t	6 others
ORIGIN					
Query Match		28.1%	Score 107;	DB 53;	Length 463;
Best Local Similarity		66.8%	Pred. No. 1.37e-176;		
Matches	219;	Conservative	0;	Mismatches 109;	Indels 1; Gaps 1;

[illegible]

RESULT	15	
ID	HS34210	standard; RNA; EST; 332 BP.
AC	T29342;	
DT	09-JAN-1995 (Rel. 42, Created)	
DE	08-SEP-1995 (Rel. 45, Last updated, Version 2)	
DD	EST71781 Homo sapiens cDNA 5' end similar to immunoglobulin kappa	
DE	light chain, V region (GS:M29469) (HT:3066).	
EST.		
KW	OS Homo sapiens (human)	
OS	OS Homo sapiens (human)	
OC	OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;	
OC	Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.	
RN	[1]	
RP	1-332	
RA	Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,	
RA	Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,	
RA	White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,	
RA	Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,	
RA	FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geophagen N.S.M.,	
RA	Glocke A., Gnehm C.L., Hanna M.C., Heblom E., Hinkle Jr P.S.,	
RA	Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,	

Search completed: Mon Jul 8 08:57:00 1996
Job time : 185 secs.

RA	Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
RA	Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
RA	Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
RA	Weidman J.F., Li Y., Bedharik D.P., Cao L., Cepeda M.A.,
RA	Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,
RA	Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
RA	Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
RA	Meisner P.S., Olsen H., Raymond L., Wei Y.F., Wang J., Xu C.,
RA	Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
RA	Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;
RT	"Initial Assessment of Human Gene Diversity and Expression
RT	Patterns Based Upon 52 Million Basepairs of cDNA Sequence";
RL	Unpublished.
CC	Other_ESTS: THC22876 Contact: Venter, JC The Institute for Genomic
CC	Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056
CC	Fax: 3018699423 Email: tdbinfo@db.tigr.org For clone availability,
CC	additional sequence and expression information related to this EST,
CC	please contact the TIGR Database (tdbinfo@db.tigr.org). NCBI gi:
CC	611440
EH	Location/Qualifiers
EH	
FT	1..332
FT	/organism="Homo sapiens"
FT	/note="human"
FT	<1..>332
FT	mrna
FT	
SO	Sequence 332 BP; 75 A; 100 C; 74 G; 76 T; 7 other;

Query Match	26.2%;	Score 100;	DB 118;	Length 332;
Best Local Similarity	66.5%;	Pred. No. 4.69e-161;		
Matches	208;	Conservative	0;	Mismatches 103;
			Indels	2;
			Gaps	2;

Db	10	atggaagcccaagctcgaagttctctctctgctactctgggtcccaagatcacacaggga	69
Qy	1	ATGGTGCTCTCAGCTTCCTGGCTCTCCTGTGCTCTGTTTCAAGGTACCATGATGT	60
Db	70	gaaattntttgacacagctccagccaccctgtntttgntccaggggaaagagccacc	129
Qy	61	GATATCCAGATGACACAGCTACATCTCCCTGTCTGCCCTCTCTGGGACAGACAGTCCAC	120
Db	130	ctctctcgagggccagtcagactgttagaacctactagcttgttaccacagaacacct	189
Qy	121	ATCAGTTTCGAGGCAAGTCAGGACATTACGACTATTTTAACTGGTATCAGCAGAAACCA	180
Db	190	ggccaggctccagggctctcatctatgatgcataccaaaggccactggcatccccagcc	249
Qy	181	GATGGACATATTAACTCTGTACTACTACATCAAGATTACACTCAGAGTGCCATCA	240
Db	250	aggttcagtgccagtggggtctnngacagactttccactctttnaccatcagcacctc	309
Qy	241	AGGTTTCAGTGGCAGTGGGCTCGGAACAGATTATT-CTCT-CACCATTTAAACACCTGGAGC	298
Db	310	ctgaagattttgc	322
Qy	299	AAGACAGATTGC	311

Search completed: Mon Jul 8 08:57:00 1996
Job time : 185 secs.

WPS RELEASE

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

WPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:57:18 1996; MasPar time 281.30 Seconds
Tabular output not generated. 1034.412 Million cell updates/sec

Title: >US-08-137-117B-30

Description: (1-411) from US08137117B.seq

Perfect Score: 411

N.A. Sequence: 1 ATGAGAGTGGTGGATTCTTTT.....CCTCAGTCACGCTCTCTCA 411
Comp: TACTCTCAGCTACTAGAAAA.....GGAGTCAGTGGCAGAGGT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 264399 seqs, 333985056 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-new1

1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN
9:PRI1 10:PRI2 11:PRI3 12:PRO1 13:PRO2 14:ROD 15:SYN
16:UNC 17:VRT 18:VIR

Database: genbank91

19:BCT1 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7
26:INV1 27:INV2 28:INV3 29:INV4 30:INV5 31:MAM1 32:MAM2
33:PA1 34:PA2 35:PA3 36:PHG 37:PLN1 38:PLN2 39:PLN3
40:PLN4 41:PLN5 42:PLN6 43:PLN7 44:PRI1 45:PRI2 46:PRI3
47:PRI4 48:PRI5 49:PRI6 50:PRI7 51:PRI8 52:PRI9 53:ROD1
54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD6 59:ROD7 60:STR
61:SYN 62:UNA 63:VRT1 64:VRT2 65:VRT3 66:VRT4 67:VRT5
68:VRT6 69:VRT1 70:VRT2 71:VRT3

Database: genbank-new11

72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN
79:PRI1 80:PRI2 81:PRI3 82:ROD 83:STR 84:SYN 85:UNA
86:VRT 87:VRT

Database: u-emb144_91

88:part1

Statistics: Mean 10.250; Variance 3.740; scale 2.741

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	330	80.3	408 56	MUSIGHDOA	Mouse Ig rearranged H	0.00e+00
2	323	78.6	399 56	MUSIGHDOB	Mouse Ig rearranged H	0.00e+00
3	319	77.6	450 54	MMIGVHR2	Mouse mRNA for immuno	0.00e+00
4	314	76.4	417 54	MMU05284	Mus musculus BALB/c/J	0.00e+00
5	313	76.2	402 56	MUSIGHDOC	Mouse Ig rearranged H	0.00e+00
6	307	74.7	460 56	MUSIGHXX	Mouse Ig rearranged g	0.00e+00
7	297	72.3	485 56	MUSIGHAAC	Mouse Ig rearranged g	7.50e-298
8	289	70.3	358 57	MUSOHP138G	Mus musculus mRNA for	1.20e-288
9	284	69.1	358 57	MUSOHP7D7G	Mus musculus mRNA for	6.68e-283
10	284	69.1	434 56	MUSIGHNUL1	Mus musculus germline	6.68e-283
11	282	68.6	492 56	MUSIGHGCK	Mouse Ig rearranged m	1.33e-280
12	279	67.9	357 56	MUSIGLAM	Mouse IgM H-chain lam	3.70e-277
13	274	66.7	402 56	MUSIGHNOH	Mouse Ig active heavy	2.03e-271
14	272	66.2	470 56	MUSIGHXY	Mouse Ig rearranged g	4.00e-269
15	272	66.2	503 56	MUSIGHAAO	Mouse Ig rearranged g	4.00e-269
16	272	66.2	702 56	MUSIGG4014	Mus musculus rearrang	4.00e-269
17	271	65.9	351 56	MUSIGHJY	Mouse Ig active heavy	5.62e-268
18	271	65.9	358 57	MUSOHP57G	Mus musculus mRNA for	5.62e-268
19	268	65.2	348 54	MMRNA246	M.musculus (BALB/c) I	1.55e-264
20	265	64.5	342 56	MUSIGHAAG	Mouse Ig rearranged h	4.25e-261
21	263	64.0	348 56	MUSIGHACW	Mouse Ig H-chain mRNA	8.33e-259
22	262	63.7	358 57	MUSOHP19G	Mus musculus mRNA for	1.17e-257
23	259	63.0	502 56	MUSIGHNUL	Mus musculus rearrang	3.18e-254
24	257	62.5	439 56	MUSIGHDS	Mouse Ig active mu-ch	6.20e-252
25	256	62.3	417 14	MM16690	Mus musculus Ig heavy	8.64e-251
26	256	62.3	417 82	MMU16690	Mus musculus Ig heavy	8.64e-251
27	255	62.0	484 53	MMIGAM32	Mouse rearranged V(H)	1.21e-249
28	254	61.8	342 56	MUSIGHZ2	Mouse IgG-2a anti-p-a	1.68e-248
29	254	61.8	826 61	XXU05272	Synthetic construct c	1.68e-248
30	252	61.3	342 59	S54194	immunoglobulin heavy	3.26e-246
31	248	60.3	339 55	MMU25121	Mus musculus anti-eta	1.22e-241
32	248	60.3	408 56	MUSIGHCA	Mouse Ig family 36-60	1.22e-241
33	246	59.9	342 56	MUSIGHAAA	Mouse IgG-1 anti-p-az	2.36e-239
34	243	59.1	351 54	MMU15297	Mus musculus immunogl	6.31e-236
35	242	58.9	358 59	S74721	Ig VH-anti-human tran	8.75e-235
36	241	58.6	405 14	MMU16687	Mus musculus Ig heavy	1.21e-233
37	241	58.6	405 82	MMU16687	Mus musculus Ig heavy	1.21e-233
38	240	58.4	288 59	S77976	Ig Vgam3.2-anti-human	1.68e-232
39	240	58.4	318 53	MMIGH11	M.musculus mRNA (L20-	1.68e-232
40	240	58.4	336 56	MUSIGHZK	Mouse IgG-1 anti-p-az	1.68e-232
41	239	58.2	294 56	MUSIGHAAX	Mouse Ig gamma-chain	2.33e-231
42	238	57.9	318 56	MUSIGHZ9	Mouse IgG-1 anti-p-az	3.22e-230
43	238	57.9	354 55	MMVHMRB9	M.musculus mRNA for I	3.22e-230
44	237	57.7	340 54	MMRNA1VHC	M.musculus mRNA for i	4.45e-229
45	237	57.7	428 56	MUSIGHME7A	Mus musculus monoclon	4.45e-229

ALIGNMENTS

RESULT 1	MUSIGHDOA	408 bp	mRNA	ROD	28-APR-1995
LOCUS	Mouse Ig rearranged H-chain mRNA V-region, 5' end of cds.				
DEFINITION	Mouse Ig rearranged H-chain mRNA V-region, 5' end of cds.				
ACCESSION	L20961				
KEYWORDS	V-region; anti-HLA antibody; antibody; immunoglobulin heavy chain; monoclonal antibody; processed gene.				
SOURCE	Mus musculus (strain BALB/c, sub species domesticus) male adult hyperimmunized spleen cDNA to mRNA.				
ORGANISM	Mus musculus				

Jul 8 08:51

US-08-137-117B-30.rge

3

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 408)
AUTHORS Iwasaki, Y., Takabatake, H., Shinji, T., Monestier, M. and Ferrone, S.
TITLE Structural profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic system

JOURNAL Eur. J. Immunol. 24 (11), 2874-2881 (1994)

MEDLINE 95045941

COMMENT NCBI gi: 309344

FEATURES Location/Qualifiers

source
1..408
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/cell_type="hybridoma"
/dev_stage="adult"
/sequenced_mol="cDNA to mRNA"
/sex="male"
/tissue_type="hyperimmunized spleen"
1..43
1..>408
/standard_name="anti-HLA-DQ3 monoclonal antibody"
/note="NCBI gi: 309345"
/codon_start=1
/product="immunoglobulin heavy chain"
/translation="MRVLLILLHLFTAPGCLISDVQLQESGRLVKSQSLSLCTVTG
YSITSDHANWIRQFPCKLEWNGYITYSGTSNNPSIKRSITRDTSKNQFFLQIN
SVTTEDTATYYCAKRWGATYYWGQTLTVSS"
44..348
349..367
368..408

exon

CDS

BASE COUNT 99 a 109 c 92 g 108 t

ORIGIN

Query Match 80.3%; Score 330; DB 56; Length 408;
Best Local Similarity 92.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 99 a 109 c 92 g 108 t

ORIGIN

Query Match 80.3%; Score 330; DB 56; Length 408;
Best Local Similarity 92.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 99 a 109 c 92 g 108 t

ORIGIN

Query Match 80.3%; Score 330; DB 56; Length 408;
Best Local Similarity 92.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 99 a 109 c 92 g 108 t

ORIGIN

Query Match 80.3%; Score 330; DB 56; Length 408;
Best Local Similarity 92.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 99 a 109 c 92 g 108 t

ORIGIN

Query Match 80.3%; Score 330; DB 56; Length 408;
Best Local Similarity 92.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 30; Indels 3; Gaps 3;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 99 a 109 c 92 g 108 t

ORIGIN

Jul 8 08:51

US-08-137-117B-30.rge

4

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE 1 (bases 1 to 399)
AUTHORS Iwasaki, Y., Takabatake, H., Shinji, T., Monestier, M. and Ferrone, S.
TITLE Structural profile of idiotype, anti-idiotype and anti-anti-idiotype monoclonal antibodies in the HLA-DQ3 antigenic system

JOURNAL Eur. J. Immunol. 24 (11), 2874-2881 (1994)

MEDLINE 95045941

COMMENT NCBI gi: 309346

FEATURES Location/Qualifiers

source
1..399
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/cell_type="hybridoma"
/dev_stage="adult"
/sequenced_mol="cDNA to mRNA"
/sex="male"
/tissue_type="hyperimmunized spleen"
1..43
1..>399
/standard_name="anti-HLA-DQ3 monoclonal antibody"
/note="NCBI gi: 309347"
/codon_start=1
/product="immunoglobulin heavy chain"
/translation="MRVLLILLHLFTAPGCLISDVQLQESGRLVKSQSLSLCTVTG
YSITSDHANWIRQFPCKLEWNGYITYSGTSNNPSIKRSITRDTSKNQFFLQIN
SVTTEDTATYYCAKRWGATYYWGQTLTVSA"
44..348
349..361
362..399

exon

CDS

BASE COUNT 93 a 107 c 94 g 105 t

ORIGIN

Query Match 78.6%; Score 323; DB 56; Length 399;
Best Local Similarity 96.3%; Pred. No. 0.00e+00;
Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 93 a 107 c 94 g 105 t

ORIGIN

Query Match 78.6%; Score 323; DB 56; Length 399;
Best Local Similarity 96.3%; Pred. No. 0.00e+00;
Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 93 a 107 c 94 g 105 t

ORIGIN

Query Match 78.6%; Score 323; DB 56; Length 399;
Best Local Similarity 96.3%; Pred. No. 0.00e+00;
Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 93 a 107 c 94 g 105 t

ORIGIN

Query Match 78.6%; Score 323; DB 56; Length 399;
Best Local Similarity 96.3%; Pred. No. 0.00e+00;
Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 93 a 107 c 94 g 105 t

ORIGIN

Query Match 78.6%; Score 323; DB 56; Length 399;
Best Local Similarity 96.3%; Pred. No. 0.00e+00;
Matches 336; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Db 1 atgagagtgtatcttttggctgttcacagccttctcgtgtatcctgtcgtatgtg 60
|||||
Qy 1 ATGAGAGTGTATCTTTTGGCTGTTCCAGCCTTCTCGTGTATCCTGTCTGATGC 60
|||||

exon

exon

exon

BASE COUNT 93 a 107 c 94 g 105 t

ORIGIN

Jul 8 08:51

US-08-137-117B-30.igs

5

Db 181 ggaacaaactgagtgatggctacataactacagtggttagcactagctacaccca 240
 Qy 181 ggaacaaactgagtgatggctacataactacagtggttagcactagctacaccca 240
 Db 241 tctctcaaaagtgcagatctctatcactcgagacacatccaaagaccaggtctctcgcag 300
 Qy 241 tctctcaaaagtgcagatctctatcactcgagacacatccaaagaccaggtctctcgcag 300
 Db 301 ttgaattctgtactactgaggacagacacatattactgtgcaaat 349
 Qy 301 ttgaattctgtactactgaggacagacacatattactgtgcaaat 349

RESULT 3
 LOCUS MMIGVHR2 450 bp RNA ROD 07-MAY-1992
 DEFINITION Mouse mRNA for immunoglobulin heavy chain variable region.
 ACCESSION X05878 Y00330
 KEYWORDS constant region; Ig heavy chain; variable region.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryotes; mitochondrial eukaryotes; Metazoa/Eumycota group;
 Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
 Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
 Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
 Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 450)
 AUTHORS Grant, F. J.
 TITLE Direct Submission
 JOURNAL Submitted (31-AUG-1987) to the EMBL/GenBank/DBJ databases. Dr.
 Francis Grant, Zymogenetics, Inc., 2121 North 35th Street, Seattle,
 Wa 98103, USA
 REFERENCE 2 (bases 1 to 450)
 AUTHORS Grant, F. J., Levin, S. D., Gilbert, T. and Kindsvogel, W.
 TITLE Improved RNA sequencing method to determine immunoglobulin mRNA
 sequence
 JOURNAL Nucleic Acids Res. 15 (13), 5496 (1987)
 MEDLINE 87260030
 COMMENT NCBI gi: 52526
 FEATURES
 source
 1..450
 /organism="Mus musculus"
 /strain="ML-05"
 /cell_type="hybridoma"
 misc_feature 4..414
 /note="variable region (AA 1-137)"
 CDS 4..>450
 /note="NCBI gi: 52527"
 /codon_start=1
 /product="Vh gene product"
 /translation="MRVLLLCVITAPPGLISDVQLQESGPDVLPKPSQSLSITCTVVG
 YSITSGYTHIRQFFGNKLEWYIHYSGNDENPSLKSRLSITRDTSKNOFFLQIN
 SVTAEDATYTCARGYGYANDYWGQGTSVTVSSAKTTPPSVYPLA"
 misc_feature 415..>450
 /note="constant region (AA 138-149)"
 BASE COUNT 116 a 126 c 92 g 116 t
 ORIGIN

Query Match 77.6%; Score 319; DB 54; Length 450;
 Best Local Similarity 88.8%; Pred. No. 0.00e+00;
 Matches 365; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
 Db 4 atgagagtgctgattcttttggctgctgcacagcgtcttctggtatcctgctgctgagtg 63
 Qy 1 ATGACAGTGCTGATTCTTTTGTGCTGTTCCACAGCCTTCTCGTCTGCTGTCTGTG 60

Jul 8 08:51

US-08-137-117B-30.igs

6

Db 64 cagcttcaggagtcaggacactgacgtggtgaaacctctcactcagtcacttcactcacctgc 123
 Qy 61 CAGCTTCAGGAGTCGGGACCTGCTGCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACTGC 120
 Db 124 actgtcactggctactcactcacccagtggttatactatggcactggatccggcagtttcca 183
 Qy 121 ACTGTCACTGGCTACTCAATCACCAGTGATCATGCTGAGCTGGATCGGCGAGTTTCCA 180
 Db 184 ggaataaattggaatggatggctacatcacactacagtggttaacactgacttcacaccca 243
 Qy 181 GGAACAACACTGGAGTGGGCTACATGAAGTTACAGTGGTATACACTACCTACACACCA 240
 Db 244 tctctcaaaagtgcagatctctatcactcgagacacatccaaagaccaggtctctcgcag 303
 Qy 241 TCTCTCAAAAGTCGAATCTCTATCACTCGAGACACATCCAAAGACCAAGTTCTTCTCTACAG 300
 Db 304 ttgaattctgtactgctgagacacagccacatattactgtgcaagaggtatggttaac 363
 Qy 301 TTGAATTCTGTGACTTGGGACACGCTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
 Db 364 tactatgctatggactactgggttcaaggaacctcagtcacgtctctctcca 414
 Qy 361 ACTACGGCTATGGACTACTGGGGTCAGGACCTCAGTCACCGCTCTCTCA 411

RESULT 4
 LOCUS MMU05284 417 bp mRNA ROD 15-FEB-1995
 DEFINITION Mus musculus BALB/c/J immunoglobulin heavy chain complete variable
 region (Igh) mRNA, partial cds.
 ACCESSION U05284
 KEYWORDS .
 SOURCE mouse.
 ORGANISM Mus musculus
 Eucaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
 Eutheria; Rodentia; Myomorpha; Muridae; Mus.
 REFERENCE 1 (bases 1 to 417)
 AUTHORS Tempest, P. R., White, P., Buttle, M., Carr, F. J. and Harris, W. J.
 TITLE Humanized and chimerized monoclonal antibodies against the
 glycoprotein qB of human cytomegalovirus
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 417)
 AUTHORS Tempest, P. R.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-1994) Phillip R. Tempest, ICOS Corporation, 22021
 20th Ave SE, Bothell, WA 98021, USA
 COMMENT NCBI gi: 463457
 FEATURES
 source
 1..417
 /clone_lib="Lambda HCV37"
 /strain="BALB/c/J"
 /organism="Mus musculus"
 /cell_line="HCV37"
 /cell_type="hybridoma"
 /tissue_type="hyperimmunized spleen"
 1..>417
 /gene="Igh"
 /note="NCBI gi: 514241"
 /codon_start=1
 /evidence=experimental
 /product="anti-cytomegalovirus-qB immunoglobulin heavy
 chain variable region"
 /translation="MRVLLILMLFTAFPGCILSDVQLQESGPDVLPKPSQSLSITCTVVG
 YSITSDYAMNIRQFFGNKLEWGMGFIYSYSGSTISPSLESRLSVTRDTSKNQFFLQLY

Jul 8 08:51

US-08-137-117B-30.gpg

7

SVTTEDTATYTCANMITSAYWDFYWGAGTTTVSS"

seq_peptide 1..54
/gene="Igh"
mat_peptide 55..417
/gene="Igh"
/evidence=experimental

BASE COUNT 94 a 111 c 98 g 114 t
ORIGIN

Query Match 76.4%; Score 314; DB 54; Length 417;
Best Local Similarity 95.4%; Pred. No. 0.00e+00;
Matches 330; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Db 1 atgagagctgctattcttttggctgttcacagcctttctggtatcctgtctgatgtg 60
|||||
Qy 1 ATGAGAGCTGCTGATTTCTTTTGGCTGTTACAGCCTTCTCGGTATCTGTCTGATGTG 60
Db 61 caggttcaggagtcggagcctggctggtgaacettctcagtcctctgtccctcacctgc 120
|||||
Qy 61 CAGGCTTCAGGAGTCGGGACCTGCTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
Db 121 actgtcaactggctactcaatcaccagtgattatgctggaaactggtacccgagtttcca 180
|||||
Qy 121 ACTGTCACTGGGTACTCAATCACCAGTGATGCTGCTGGAGCTGGATCCGGCAGTTTCCA 180
Db 181 ggaacaaaactggagtgatgggtttcataagctacagtggttagcactagctacacaccca 240
|||||
Qy 181 GGAAACAACTGGAGTGGATGGGCTACATAGTTACAGTGGTATCATTCTACCTACAAACCCA 240
Db 241 tctctcgaagtccaatcctctgtcactcagagacacatccaagaacagcttctctctcag 300
|||||
Qy 241 TCTCTCAAAAGTCGAATCTCTATCATCTCGAGACACATCCAAGACCACTTCTTCTACAG 300
Db 301 ttgtattctgtgaactgaggagacagcagcacatattactgtgcaa 346
|||||
Qy 301 TTGAATTTCTGTACTCTGGGACACGCTCCACATATTACTGTGCAAA 346

RESULT 5
LOCUS MUSIGHQOC 402 bp mRNA ROD 28-APR-1995
DEFINITION Mouse Ig rearranged H-chain mRNA V-region, 5' end of cds.
ACCESSION L20957
KEYWORDS V-region; anti-HLA antibody; antibody;
immunoglobulin heavy chain; monoclonal antibody; processed gene.
SOURCE Mus musculus (strain BALB/c, sub species domesticus) male adult
hyperimmunized spleen cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 402)
AUTHORS Iwasaki,Y., Takabatake,H., Shinji,T., Monestier,M. and Perrone,S.
TITLE Structural profile of idiotype, anti-idiotypic and
anti-anti-idiotypic monoclonal antibodies in the HLA-DQ3 antigenic
system

JOURNAL Eur. J. Immunol. 24 (11), 2874-2881 (1994)
MEDLINE 95045941
COMMENT NCBI gi: 309348
FEATURES Location/Qualifiers
source 1..402
/organism="Mus musculus"
/strain="BALB/c"
/sub species="domesticus"
/cell_line="S01"
/cell_type="hybridoma"

Jul 8 08:51

US-08-137-117B-30.gpg

8

/dev_stage="adult"
/sequenced_mol="cDNA to mRNA"
/sex="male"
/tissue_type="hyperimmunized spleen"
<1..43
1..>402
/standard_name="anti-HLA-DQ3 monoclonal antibody"
/note="NCBI gi: 309349"
/codon_start=1
/product="immunoglobulin heavy chain"
/translation="MRVLILLILWLFATPGLISDVQLQESGPIVRSQSLSLCTVTG
YSITSDYAMNIRFPFGKLEWGYISYSGSTGYNPSIKRSISITRDTSRNQFILOIN
SVTTEDTATYTCARFYDFYWGQGTTLTVSS"
44..348
349..359
360..402
BASE COUNT 93 a 111 c 93 g 105 t
ORIGIN

Query Match 76.2%; Score 313; DB 56; Length 402;
Best Local Similarity 95.1%; Pred. No. 0.00e+00;
Matches 330; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Db 1 atgagagctgctattcttttggctgttcacagcctttctggtctctgtctgatgtg 60
Qy 1 ATGAGAGCTGCTGATTTCTTTTGGCTTTCACAGCCTTCTCGGTATCTGTCTCATGTG 60
Db 61 caggttcaggagtcggagcctggctggtgagacctctcagtcctctgtccctcacctgc 120
|||||
Qy 61 CAGGCTTCAGGAGTCGGGACCTGCTCCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120
Db 121 actgtcaactggctactcaatcaccagtgattatgctggaaactggatccggcagttcca 180
|||||
Qy 121 ACTGTCACTGGCTTACTCAATCACCAGTGATGCTGCTGGAGCTGGATCCGGCAGTTTCCA 180
Db 181 ggaacaaaactggagtgatgggtctacataagctacagtggttagcactggtctacaccca 240
|||||
Qy 181 GGAAACAACTGGAGTGGATGGGCTACATAGTTACAGTGGTATCATTCTACCTACAAACCCA 240
Db 241 tcgctcaaaagtgaatctctatcactcgagacacatccaagaacagttctctctcag 300
|||||
Qy 241 TCTCTCAAAAGTCGAATCTCTATCATCTCGAGACACATCCAAGACCACTTCTTCTACAG 300
Db 301 ttgaattctgtgactactgaggacagcagccacatattactgtgcaag 347
|||||
Qy 301 TTGAATTTCTGTACTCTGGGACACGCTCCACATATTACTGTGCAAG 347

RESULT 6
LOCUS MUSTCHXX 460 bp mRNA ROD 26-MAR-1994
DEFINITION Mouse Ig rearranged gamma-chain mRNA, clone AN02g.
ACCESSION M19894 J03832
KEYWORDS C-region; immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.
SOURCE Mus musculus (strain BALB/c, sub species domesticus) cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 54)
AUTHORS Rule,G.S.
JOURNAL Unpublished (1988) Stanford U., Chem. Dept., Stanford CA 94305
REFERENCE 2 (bases 55 to 460)
AUTHORS Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
TITLE Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-

JOURNAL bodies for NMR studies
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
COMMENT 88234486
Draft entry and computer-readable sequence [2] kindly submitted by
G.Rule, 20-JUL-1988.

NCBI gi: 196225
source 1..460
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/cell_type="mature B cell"
/sequenced_mol="cDNA to mRNA"
sig_peptide 55..108
/codon_start=1
CDS 55..>460
/note="precursor; NCBI gi: 554044"
/codon_start=1
/product="immunoglobulin gamma-chain"
/translation="MRVLILLFLTFAPGILSDVQLQESGPIVKEPSQSILCTVTYG
YSITSDYAMNIRQFPNGKLEWMGMYSGSTRNPSLRISITRDTSKNQFFLIQLK
SVTTEDTATYFCARGPLAYWGQCTQVSVEAK"
mat_peptide 109..>460
/codon_start=1
/product="immunoglobulin gamma-chain"
BASE COUNT 112 a 116 c 114 g 118 t
ORIGIN

Query Match 74.7%; Score 307; DB 56; Length 460;
Best Local Similarity 94.2%; Pred. No. 0.00e+00;
Matches 327; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Db 55 atgagagtcgtattcttttggctgttcacagcctttctcgtatcctgtcgtatggtg 114
|||||
Qy 1 ATGAGAGTCGTGANTCTTTTGGCTGCTCACAGCCTTCTCGGTATCTCTGTGATGTG 60

Db 115 cagcttcaggagtcgggaactgacctggtgaacaccttcacgtctcagtcacctcctgc 174
|||||
Qy 61 CAGCTTCAGGAGTCGGGACCTGTCTGCTGAGCCTTCTCAGTCTCTGCTCCCTCACCTGC 120

Db 175 actgtcactggctactcaatcaccagtgattatgcttggaaactggatccggcaggtttcca 234
|||||
Qy 121 ACTGTGACTGGCTACTCATACACAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCCA 180

Db 235 ggaacaaaattggagtgatgggtacatgagctacagtggaagcactaggtacaaacca 294
|||||
Qy 181 GGAACAAAATGGAGTGGATGGGTACATAAGTTACAGTGGTATCATTACTACAAACCCA 240

Db 295 tctctcagaagtcgaactctatcactcgagacacatccaagaaccagttcttctcgag 354
|||||
Qy 241 TCTCTCAAAGTCCGAATCTCTATCATCCGAGACATCCAAGACAGATTCTTCTCTACAG 300

Db 355 ttgaagtccagtgactactcaggaacacagccacatatatttctgtgcaag 401
|||||
Qy 301 TTGAATTCGTGTACTCTGCGGACAGCTCCACATATTACTGTGTCAG 347

RESULT 7
LOCUS MUSIGHAC 485 bp mRNA ROD 26-MAR-1994
DEFINITION Mouse Ig rearranged gamma-chain mRNA, clone AN07g.
ACCESSION M19899 J03832
KEYWORDS C-region; immunoglobulin gamma-chain; immunoglobulin heavy chain;
processed gene.

SOURCE Mouse (strain BALB/c) mature B cell, cDNA to mRNA, clone AN07g.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 56)
AUTHORS Rule,G.S.
JOURNAL Unpublished (1988) Stanford U., Chem. Dept., Stanford CA 94305
REFERENCE 2 (bases 57 to 485)
AUTHORS Leahy,D.J., Rule,G.S., Whittaker,M.M. and McConnell,H.M.
TITLE Sequence of 12 monoclonal anti-dinitrophenyl spin-label anti-
bodies for NMR studies
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85, 3661-3665 (1988)
MEDLINE 88234486
COMMENT Draft entry and computer-readable sequence [2] kindly submitted by
G.Rule, 20-JUL-1988.

NCBI gi: 194558
source 1..485
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/cell_type="mature B cell"
/sequenced_mol="cDNA to mRNA"
sig_peptide 57..110
/codon_start=1
CDS 57..>485
/note="precursor; NCBI gi: 466287"
/codon_start=1
/product="immunoglobulin gamma-chain"
/translation="MRVLILLCLFAPFGILSDVQLQESGPIVKEPSQSILCTVTYG
YSITSGYSWMIRQFPCHKLEMGYIHYSGSTRNPSLRISITRDTSKNQFFLIQIN
SVTTEDTATYCARVYVYGGSSYWFAYWGQCTLVTSAAK"
mat_peptide 111..>485
/codon_start=1
/product="immunoglobulin gamma-chain"
BASE COUNT 119 a 125 c 109 g 132 t
ORIGIN

Query Match 72.3%; Score 297; DB 56; Length 485;
Best Local Similarity 92.8%; Pred. No. 7.50e-298;
Matches 322; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db 57 atgagagtcgtattcttttggctgttcacagcctttctcgtatcctgtcgtatggtg 116
|||||
Qy 1 ATGAGAGTCGTGATCTTTTGGCTGTTACAGCCTTCTCGGTATCTCTGTGATGTG 60

Db 117 cagcttcaggagtcaggacctgacctggtgaacaccttcacgtcacttcacacctgc 176
|||||
Qy 61 CAGCTTCAGGAGTCGGGACCTGTCTGCTGAGCCTTCTCAGTCTCTGTGCTCCCTCACCTGC 120

Db 177 actgtcactggctactccatcaccagtggttatagctggcactggatccggcaggtttcca 236
|||||
Qy 121 ACTGTGACTGGCTACTCAATCACCACTGATCATCCCTGGAGCTGGATCCGGCAGTTTCCA 180

Db 237 ggaacaaaactggaatggatgggtacatcacactacagtggttagcactaacacaaacca 296
|||||
Qy 181 GGAACAAAATGGAGTGGATGGGCTACATAAGTTACAGTGGTATCATCTACTACAAACCCA 240

Db 297 tctctcaaaagtgaatctctatcactcgagacacatccaagaaccagttcttctcgag 356
|||||
Qy 241 TCTCTCAAAGTCCGAATCTCTATCATCTCGAGACATCCAAGACAGTTCTTCTCTACAG 300

Db 357 ttgaattctgtgactactcaggaacacagccacatatattctgtgcaag 403

115	ACCTGC	ACTCTG	CTACTG	CGCTACTCAAT	CACCA	SGTGCATC	GCCTGG	AGTGGA	TCCGGCG	174
121	tittcagg	aaacaa	actcgag	tggatggg	ctacataa	caactaca	aggggtg	gcac	tggttac	180
175	TTTCCG	GAACAA	CAACTG	SGATGG	CTAC	TAAAGTT	CACAGT	GGTATC	CACACCTAC	234
181	aaccat	ctctc	aaagt	tcgaatct	ctctc	actcgag	acacatc	caagac	caggttttc	240
235	AACCA	CACTCT	CAA	AAAGTC	GAATCT	TATCACT	CAGAC	ACATCC	GAACAGCTTCTC	294
241	ctgcaatt	gaattct	gtgac	ccactgag	gacacg	ccacatatt	actctgt	caagag	ggttaat	300
295	CTACAG	TGAA	TTCTG	TGCTACT	CGGG	GAACAG	CTCCACAT	TATTACT	GTGCAAGATCCC	353
301	cgttact	actatg	-ct	atg	gaact	actgggt	caagaa	caacct	cagtcac	357
354	AGCTCG	GACTAC	GGGTAT	TGGACT	TACTGG	GGTCAAG	GAACAACT	CAGTCA	CCGCTTCTCA	411

SEGMENT	1 of 2
SOURCE	Mus musculus (strain BALB/c, sub-species domesticus) liver DNA.
ORGANISM	Mus musculus
	Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

REFERENCE
1 (bases 1 to 434)
AUTHORS
Komori, T., Sugiyama, H. and Kishimoto, S.
TITLE
A novel VHDH to JH joining that induces H chain production in an
Ig-null immature B cell line
J. Immunol. 143 (3), 1040-1045 (1989)
MEDLINE
89309739

NCBI gi: 341844	Location/Qualifiers
source	1..434

```

/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/germline
/sequenced_mol="DNA"
/tissue_type="liver"
<1.10
exon

```

```

/sequn_data=1
/product="immunoglobulin heavy chain"
/translation="AFGILSDVQLQESGPGVKRPSQSLSTCTVTCYSTSDYANW
INQPPGNKLEWNGYISYSTSPNPILKRSITSDT7SKNQFFIQLINSVTGGVTTTR
VI11"

```

```
sig_peptide      join(<1..10,93..103)
                  /gene="Igh"
                  /map="12"
                  /codon_start=1
CDS              join(<1..10,93..366,
```

CDS	<p> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/note="NCBI gi: 550492"</code> <code>/codon_start=1</code> <code>/product="immunoglobulin heavy chain"</code> <code>/translation="AFPGILSDVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYANRW</code> <code>IRQFFGNKLEWMCYISYSGTSYNPSLKSRISITRDTSKNOFFLQLNSVTTRGGYDDAT</code> <code>GYF"</code> </p>	<p> <code>join(<1..10,93..371,401..434)</code> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/note="NCBI gi: 550491"</code> <code>/codon_start=1</code> <code>/product="immunoglobulin heavy chain"</code> <code>/translation="AFPGILSDVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYANRW</code> <code>IRQFFGNKLEWMCYISYSGTSYNPSLKSRISITRDTSKNOFFLQLNSVTTRGGYDDAT</code> <code>ATGTY"</code> </p>
CDS	<p> <code>join(<1..10,93..365,401..434)</code> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/note="NCBI gi: 550493"</code> <code>/codon_start=1</code> <code>/product="immunoglobulin heavy chain"</code> <code>/translation="AFPGILSDVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYANRW</code> <code>IRQFFGNKLEWMCYISYSGTSYNPSLKSRISITRDTSKNOFFLQLNSVTTRGGYDDAT</code> <code>GTT"</code> </p>	<p> <code>11..92</code> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/number=1</code> <code>93..366</code> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/note="alternatively spliced exon"</code> <code>/number=2</code> <code>93..365</code> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/note="alternatively spliced exon"</code> <code>/number=2</code> <code>93..371</code> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/note="alternatively spliced exon"</code> <code>/number=2</code> <code>93..364</code> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/note="alternatively spliced exon"</code> <code>/number=2</code> <code>join(104..366,401..434)</code> <code>/partial</code> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/codon_start=1</code> <code>/product="immunoglobulin heavy chain"</code> <code>join(104..371,401..434)</code> <code>/partial</code> <code>/gene="Igh"</code> <code>/map="12"</code> <code>/codon_start=1</code> <code>/product="immunoglobulin heavy chain"</code> <code>join(104..365,401..434)</code> <code>/partial</code> </p>
intron		
exon		
exon		
exon		
mat_peptide		
mat_peptide		
mat_peptide		

Db 193 tctctgtccctcaactgcaactgctcaactggctactcaatcaccagtgattatgcttgaac 252
|||||
Qy 103 TCTCTGTCCCTCAGCTGCAGTGTCTACTGGGTACTCATACACAGTGATCGCTGGAGC 162
|||||
Db 253 tggatccggcaggttccaggagaacaaactggagtggatgggtcacataaagctacagtggt 312
|||||
Qy 163 TGGATCCGGCAGCTTCCAGGAACAACTGGAGTGGATGGGTACATAAGTTACAGTGGT 222
|||||
Db 313 agcactagctcaaacccatctctcaaaagtcgaaatctctatcaactcgagacacatccaag 372
|||||
Qy 223 ATCACTACTCAACACCATCTCTCAAAAGTCGAATCTATCACTCCAGACACATCCAAAG 282
|||||
Db 373 aaccagttctctgcagttgaattctgcgactactgagacacagcacatattactgt 432
|||||
Qy 283 AACCAGTTCTTCTCTACAGTTGAATTTCTGCTACTCTGGGACACGTCACATATTAAGTGT 342
|||||
Db 433 gcaaga 438
|||||
Qy 343 GCAAGA 348

RESULT 12
LOCUS MUSIGLAM 357 bp mRNA ROD 15-DEC-1988
DEFINITION Mouse IgM H-chain lambda rearranged anti-Dns hybridoma VDJ1 region
from family 36-60 mRNA.
ACCESSION M15231
KEYWORDS C-region; V-region; immunoglobulin heavy chain;
immunoglobulin lambda; immunoglobulin lambda-2.
SOURCE Mouse (strain Balb/c) hybridoma mRNA, clone DF8-611.1.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 357)
AUTHORS Chua, M.-M., Goodgal, S.H. and Karush, F.
TITLE Germ-line affinity and germ-line variable-region genes in the B
cell response
JOURNAL J. Immunol. 138, 1281-1288 (1987)
MEDLINE 87110678
COMMENT NCBI gi: 197675
FEATURES
source
1..357
Location/Qualifiers
/organism="Mus musculus"
BASE COUNT 87 a 101 c 82 g 87 t
ORIGIN Chromosome 16.

Query Match 67.9%; Score 279; DB 56; Length 357;
Best Local Similarity 89.1%; Pred. No. 3.70e-277;
Matches 318; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Db 1 gatgtcagcttcaaggagccggagactggctggtaaaccttctcagctctgtccctc 60
|||||
Qy 55 GATGTGCAGCTTCAAGAGTGGGACCTCTCTGGTGAAGCTTCTCAGTCTGTGCTCCTC 114
|||||
Db 61 acctgcactgtcactggctactcaatcaccagtcagtgattatgcttggaaactggatccggag 120
|||||
Qy 115 ACCTGCAGTCTACTGGCTACTCATACACAGTATCATATCGCTGGAGCTGGATCCGGCAG 174
|||||
Db 121 ttctcaggaaacaaactggagtggtgggtacataaagctacagtggtgagcactagctac 180
|||||
Qy 175 TTTCAGGAAACAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCATACCTAC 234
|||||
Db 181 aaccatctctcaaaagtcgaatctctatcaactcgagacacatccaagaaccagttctc 240
|||||

Qy 235 AACCATCTCTCAAAAGTCGAATCTATCACTCGACACATCCAGAACACGTTCTTC 294
|||||
Db 241 ctgcagtgaattctgtgactactgagagacacagccacacatattactgtcaagatgtccc 300
|||||
Qy 295 CTACAGTTCAATTTCTGTGACTTGGGGACAGTCACACATATTACTGTCAAGATCCCTA 354
|||||
Db 301 tatgattcttgactgtactgtctgtgggcagcagcagcaggtcacctgtctctca 357
|||||
Qy 355 CCTCGGAGCTACCGGTATCGACTACTGGGTCAAGGAACCTCAGTACCGCTCTCCTCA 411
|||||

RESULT 13
LOCUS MUSIGHNOH 402 bp mRNA ROD 17-SEP-1991
DEFINITION Mouse Ig active heavy-chain mRNA V-region.
ACCESSION M64137
KEYWORDS V-region; immunoglobulin heavy chain; processed gene.
SOURCE Mouse (strain BALB/c) B-cell hybridoma, cell line H146-24E9, cDNA
to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 402)
AUTHORS Caton, A.J., Stark, S.E., Kavalier, J., Staudt, L.M., Schwartz, D. and
Gerhard, W.
TITLE Many variable region genes are utilized in the antibody response of
balb/c mice of the influenza virus a/pr/8/34
JOURNAL J. Immunol. 147, 1675-1686 (1991)
MEDLINE 91349593
COMMENT Specific for influenza virus A/PR/8/34 hemagglutinin.

NCBI gi: 195701
FEATURES
source
Location/Qualifiers
1..402
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/cell_line="H146-24E9"
/cell_type="B-cell hybridoma"
/sequenced_mol="cDNA to mRNA"
CDS
1..>402
/note="NCBI gi: 195702"
/codon_start=1
/product="Ig heavy chain"
/translation="FFWCLTFAPFGLSDVQLQESGPULVKPQSLSLTCTVTGYSIT
SGYSWHWIRQFPNKLEHMGYIHYSGTKYNPISKSAISITRDTSKNOFFLQINSVTT
EDTATVYCARDDTFYDYGQCTTLTVSSAKHH"

BASE COUNT 104 a 113 c 81 g 104 t
ORIGIN
Query Match 66.7%; Score 274; DB 56; Length 402;
Best Local Similarity 91.3%; Pred. No. 2.03e-271;
Matches 303; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Db 5 ttgtgtgcctgttcacagccttctcgtgtatctgtctgtatgtcagcttcaggagtcag 64
|||||
Qy 17 TTTTGTGGCTGTTCACAGCCTTCTCGTATCTCTGTCATGTCAGCTTCAGGAGTCGG 76
|||||
Db 65 gacctgacctggtgaacacctctcagtcactcttcactcactcactgtcactgtcact 124
|||||
Qy 77 GACCTGTCTGGTGAAGCCTTCTCAGTCTCTGTCCTCACCCTGCAGTGTCTACTGGCTACT 136
|||||
Db 125 ccatcacaccagtggttatagctggcaactggatccggcagtttccaggaaacaaactggaat 184
|||||
Qy 137 CAAATCAACAGTATCATGCTCGAGCTGGATCCGGCAGTTTCCAGGAACAAACTGGAGT 196
|||||

Query Match 66.2%; Score 272; DB 56; Length 470;
Best Local Similarity 84.9%; Pred. No. 4,00e-269;
Matches 349; Conservative 0; Mismatches 59; Indels 3; Gaps 2;
Db 56 atgaagaattgagdtctgtttacactcttgacagcagcattctctgtatctctgatgata 115

[illegible]

Jul 8 08:51

US-08-137-117B-30.gc

21

/translation="MKVLSILYLLTAIPGILSDVQLQESGCLVPSQSLSLTCSTVG
YSITSGYWMWIRQFPNGKLEWGYINDGRNNYNPSLKNRISITHTDSKNQFFLKIK
SVTTEDTATYYCAREDDGYIFDYWGQSTLTWSSAKTTPPSVPLA"

mat_peptide 111..>503

/codon_start=1

/product="immunoglobulin gamma-chain"

BASE COUNT 133 a 131 c 106 g 133 t

ORIGIN

Query Match 66.2%; Score 272; DB 56; Length 503;
Best Local Similarity 84.2%; Pred.No. 4,00e-269;
Matches 347; Conservative 0; Mismatches 63; Indels 2; Gaps 2;

Db 57 atgaagatgttgagctgtgttacctgttgacagccattcctggtatccctgtctcgatgta 116

Qy 1 ATGAGAGTCTGATTCCTTTGTGGCTGTTACAGCCCTTTCTCGGTATCCTGTCTGATGTG 60

Db 117 cagcttcaggagtcaggacctggcctcgtgaaacctctcagctctgtctctcaacctgc 176

Qy 61 CAGCTTCAGAGTCGGGACCTCTCCTGGTGAAGCCTTCTCAGTCTCTGCTCACCTGC 120

Db 177 tctgtcaactggctactccaccagtggttattactggaactggatccggcaggtttcca 236

Qy 121 ACTGTCACTGGCTACTCATCACCAGTGATCATGCCCTGGAGCTGGATCGCGGAGTTTCCA 180

Db 237 ggaacaaactggaatggatgggtacataaactacgacggtgaggataactacaacca 296

Qy 181 GGAACAAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCATTACCTACAAACCA 240

Db 297 tctctcaaaactcgaatctccactcgtgacacatctaagaaccagtttttcctgaag 356

Qy 241 TCTCTCAAAAGTCCAATCTATCACTCGAGACATCCAAAGACCAAGTTTCTTCCTACAG 300

Db 357 ttgaagctcttgacaactgaggacacagctacatatattactgtgcaagagaggtatggt 416

Qy 301 TTGAATTTCTGCTACTCTGGGACACGCTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360

Db 417 tactacatcttgg-actactggggccaaggtccactctcaagtcctctcca 467

Qy 361 -ACTACGGCTATGGACTACTTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA 411

Search completed: Mon Jul 8 09:02:07 1996
Job time : 289 secs.

PT has low antigenicity and contains mouse V-region complementarity
PT Determining regions
PS Disclosure; Page 122-123; 207pp; Japanese.
CC The sequences given in Q30755-56 were used in example to illustrate
CC the production of a human antibody which recognises human
CC interleukin-6 receptor (IL-6R). The antibody comprises light (L)
CC chain and heavy (H) chain variable regions which were derived from a
CC mouse monoclonal antibody produced from the hybridoma PM1 which
CC contained the plasmids pPM-k3 and pPM-h1.
SQ Sequence 411 BP; 95 A; 114 C; 92 G; 110 T;

Query Match 100.0%; Score 411; DB 5; Length 411;
Best Local Similarity 100.0%; Pred. No. 8.03e-269;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 atgagagtgctgattcttttggctgtctcaagccttctcagtcctgtctgtctgtg 60
Qy 1 ATGAGAGTCTGATTCTTTTGGCTGTCTCAACGCTTTCCTGGTATCTGTCGATGTG 60
Db 61 cagcttcaggagtcggacactgtcctggggaagccttctcagtcctgtccctcacctgc 120
Qy 61 CAGCTTCAGGAGTCGGACCTGTCTGGTGAAGCCTTCTCAGTCTGTCTCCCTCACCTGC 120
Db 121 actgtcactggtactcaatacaccagtgatcgtcgtggagtcggagtcggagtttccaa 180
Qy 121 ACTGTCACGTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCGGCGAGTTTCCA 180
Db 181 ggaacaaactggagtggtgggtacataagttacagtggtgtatcactacacaaacca 240
Qy 181 GGAACAAACTGGAGTGGATGGGTACATAAGTTACAGTGGTATCAGTCTACCTACAAACCCA 240
Db 241 tctctcaaaagtcgaatctctatcactcagagacacatccaagaccagcttctcctacag 300
Qy 241 TCTCTCAAAGTCAATCTCTATCCTCAGACACATCCAAAGACCAGTCTCTCTCAGCAG 300
Db 301 ttgaattctgtactactgggacacgtccacatattactgtcaagatccctagctcgg 360
Qy 301 TTGAATTTCTGACTACTGCGGACACGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360
Db 361 actacgctatggactactgggtcaagaaacctcagtcacgtctctccta 411
Qy 361 ACTACGGCTATGGACTACTGCGGTCAGGAACCTCAGTACCGCTCTCCTCA 411

RESULT 2
ID Q40462 standard; DNA; 720 BP.
AC Q40462;
DT 20-AUG-1993 (first entry)
DE Fv(TU27).
KW pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;
KW heavy; beta; chain; interleukin; IL-2; receptor; inhibition;
KW immunomodulator; immunosuppressant; graft rejection; allergy;
KW autoimmune disease; leukemia; cyclosporin; ss.
OS Homo sapiens.
PN EP-539748-A.
PD 05-MAY-1993.
PF 03-SEP-1992; 116746.
PR 03-OCT-1991; JP-256335.
PA (AJIN) AJINOMOTO KK.
PI Hamuro J, Shinamura T, Taki S;
DR WPI; 93-145163/18.
DR P-PSDB; R34510.
PT Polypeptide(s) which bind H chain of human IL-2 receptors - for
PT treating inflammatory, allergic and auto-immune disorders,

PT leukaemias etc.
PS Claim 6; Page 20; 27pp; English.
CC The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express
CC polypeptides consisting only of the V regions were purified and
CC sequenced. The polypeptides are capable of binding to the beta
CC chain of IL-2 receptor and of inhibiting the binding of IL-2 to the
CC receptor. They are useful as immunomodulators and
CC immunosuppressants, e.g. to prevent graft rejection or to treat
CC inflammatory allergic and autoimmune diseases, or leukemia. Unlike
CC cyclosporin etc. they are both effective and safe.
SQ Sequence 720 BP; 186 A; 188 C; 170 G; 176 T;

Query Match 64.5%; Score 265; DB 7; Length 720;
Best Local Similarity 90.7%; Pred. No. 1.36e-164;
Matches 312; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

Db 380 agagctcggactggcctggtgaaaccttctcagtcctcctccctcacctgcactgtca 439
Qy 68 AGGAGTCGGGACCTGTCTGCTGAAGCCTTCTCAGTCTGTCTCCTCAGCTGCACGTGTCA 127
Db 440 ctggctacccaatacaccagtgattatgctgggagtcggagtcggagttccagaagaaaca 499
Qy 128 CTGGCTACTCAATCACAGTGATCATGCTGGAGCTGGATCGGCGAGTTTCCAGGAACA 187
Db 500 aactggagtgagtggtcagtaagctacagtgtagcagtcgactgactacacacccatctctca 559
Qy 188 AACTGGAGTGGATGGGCTACATATAGTTAGTGTATGACTACTACACACCATCTCTCA 247
Db 560 aaagtgcgaatctctatcagtcgagacacatccaagaccagttcttctcagttgaatt 619
Qy 248 AAGTGCATCTCTATCACTCGACACATCCAAAGAACCGTTTCTTCTAGACATTTGAAT 307
Db 620 ctgtgactactgagacacagccacatattactgtcgaagagg--tggtttccctctag- 676
Qy 308 CTGTGACTACTGCGGACCGTCCACATATTACTGTGCAAGATCCCTAGCTCGGACTACGG 367
Db 677 ctatgactactgggtcaaggaccacagtcacgtctcctca 720
Qy 368 CTATGGACTACTGCGGTCAGGAACCTCAGTACCGCTCTCCTCA 411

RESULT 3
ID Q25667 standard; cDNA; 378 BP.
AC Q25667;
DT 28-DEC-1992 (first entry)
DE Sequence of the anti-urokinase antibody kappa variable region (VK)
DE cDNA
KW Chimeric monoclonal antibody; anti-urokinase antibody; PCR;
KW antithrombotic agent; myocardial infarction therapy; ss.
OS Mus musculus.
FT Key Location/Qualifiers
FT sig_peptide 1..9
FT /*tag= a 10..378
FT mat_peptide 1..27
FT /*tag= b 18..32
FT misc_feature 1..27
FT /*tag= c
FT /label= VH01 primer
FT misc_feature 18..32
FT /*tag= d
FT /label= 5'VH1 primer
FT misc_feature 340..371
FT /*tag= e
FT /label= 3' mVH primer

FT misc feature 356..371
 FT /*tag= f
 PN /label= JH01 primer
 PD EP-491351-A.
 PR 24-JUN-1992.
 PR 17-DEC-1991; 121591.
 PR 18-DEC-1990; JP-413829.
 PR 11-NOV-1991; JP-294464.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Iwasa S, Taka H, Watanabe T, Tada H;
 DR WPI; 92-209528/26.
 DR P-PSP; R24722.
 PT Chimeric monoclonal antibodies - contain anti-human fibrin
 PT antibody light and heavy chain variable and constant for treating
 PT thrombotic conditions e.g. myocardial infarction
 PS Example; Figure 15; 87pp; English.
 CC Poly(A)+ RNA was prepd. from mouse anti-urokinase
 CC antibody-producing hybridoma UK1-3 cells. Using this poly(A) RNA as
 CC a template, an anti-urokinase antibody VK cDNA was amplified with
 CC the mC-kappa primer as primer for first strand synthesis, and the
 CC 3'mV-kappa and 5'mV-kappa primers as primers for the PCR. The
 CC amplified fragment was restriction digested and ligated into a
 CC restriction fragment of pTB1423 to give an anti-urokinase antibody
 CC VK cDNA contg. plasmid pTB1456. The sequence of this plasmid is
 CC given in Q25667. The cDNA is a functional VK gene. The sequence of
 CC the primer (mC-gamma-I) is given in Q25689.
 SQ Sequence 378 BP; 92 A; 100 C; 91 G; 95 T;

Query Match 62.3%; Score 256; DB 4; Length 378;
 Best Local Similarity 93.2%; Pred. No. 3.28e-158;
 Matches 276; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 Db 9 taagtgcaactagtgagtcggagcctggctggtgaaaccttctcagtcctctgtcctc 68
 Qy 54 TGATGTGCGAGCTTGAGGAGTCGGGACCTGTCTGTGAGCCCTTCATGCTCTGTCCT 113
 Db 69 cactgcactgtcactggctactcaatcaccagtgattatgctggaactggatccgca 128
 Qy 114 CACCTGCACCTGCTACTGGCTACTCAATACCAGTCATCATGCTGAGCTGGATCCGCA 173
 Db 129 gttccaggaaacaaactggagtgatgggtacataaactacagtggtaccactagtta 188
 Qy 174 GTTCCAGGAACAAACTGGAGTGGATGGCTACATAAGTTACAGTGTATCATCTACCTA 233
 Db 189 caaccatctcctcaaaagtgaactctctatcactcgagacacatcaataaccagtttt 248
 Qy 234 CAACCGATCTCTCAAGTGGATCTCTATCTACTCGACACATCCAGAACCACTGCTT 293
 Db 249 cctgcagtggaattctgtgactcttgaggacactgcccacatattactgtgcaagat 304
 Qy 294 CCTAGATTGAATCTGTGACTACTGGGGACACGTCACATATTACTGTGCAAGAT 349

RESULT 4
 ID Q67358 standard; DNA; 714 BP.
 AC Q67358;
 DT 27-MAR-1995 (first entry)
 DE Anti-traseolide 02/01/01 scFv.
 KW Binding protein; immobilization; chimeric protein;
 KW anchoring protein; Saccharomyces cerevisiae; pUR4143;
 KW musk fragrance; traseolide; polymerase chain reaction;
 KW PCR; amplification; primer; light chain; hybridoma; scFv;
 KW single chain antibody; monoclonal antibody; ds.
 OS Synthetic.

PN W09418330-A.
 PD 18-AUG-1994.
 PF 10-FEB-1994; E00427.
 PR 10-FEB-1993; EP-200350.
 PA (UNIL) UNILEVER NV.
 PA (UNIL) UNILEVER PLC.
 PI De Geus P, Erenken LGJ, Klis FM, Toeschka HY, Verrips CT;
 DR WPI; 94-279751/34.
 PT Immobilised binding proteins for specific cpds - obtd. by
 PT expressing chimeric proteins comprising the binding protein and a
 PT cell wall-anchoring protein in host cells
 PS Disclosure; Page 35; 78pp; English.
 CC Valuable compounds are isolated from complex mixtures by use of
 CC immobilized ligands composed of an anchoring protein and a binding
 CC protein. A gene encoding such a chimeric protein that will anchor
 CC in the cell wall of a lower eukaryote, e.g. S. cerevisiae, and which
 CC binds traseolide with high specificity, was constructed using plasmid
 CC pUR4143. This plasmid contains a gene encoding an scFv-TRAS
 CC fragment of anti-traseolide antibody 02/01/01 (Q67358) obtained by
 CC PCR amplification of hybridoma cDNA using primers Q67353-54 for
 CC the heavy chain, and primers Q67355-56 for the light chain.
 SQ Sequence 714 BP; 174 A; 188 C; 178 G; 174 T;

Query Match 62.0%; Score 255; DB 12; Length 714;
 Best Local Similarity 93.8%; Pred. No. 1.68e-157;
 Matches 273; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 Db 1 ctgaggagctggacctggcctggctgaaaccttctcagtcctctgtcctcactgcact 60
 Qy 64 CTTCCAGAGTCGGGACCTGCTCTGCTGAAGCCTTCTCAGTCTCTGCTCCTCAGCTGCACT 123
 Db 61 gtcaactgctactcaatcaccagtgatttgcctggaactggatccggcagtttccaggga 120
 Qy 124 GTCACTGGCTACTCAATCACCAGTGATCATGCTGGAGCTGGATCCGGCAGTTTCACAGA 183
 Db 121 aaccaactggagtgatggctacataaagctacagtggtagcactagctacaacccatct 180
 Qy 184 AACAACTGGAGTGGATGGGCTACATAGTTACAGTGGTATCATCTACACACCCATCT 243
 Db 181 ctcaaaagtcgaatctctcactcgagacacatccaagaaccagttcttctcagcttg 240
 Qy 244 CTCAAAAGTCCGAATCTTATCATCTCGAGACACATCCAAAGAACCAAGTTCTTCTACAGTTG 303
 Db 241 aattctgactactgagacacagccacatattactgtgcaacgtcccta 291
 Qy 304 AATTCTGTGACTACTGGGACACGTCACATATTACTGTGCAAGATCCCTA 354

RESULT 5
 ID Q80291 standard; DNA; 639 BP.
 AC Q80291;
 DT 08-JUL-1995 (first entry)
 DE Monoclonal antibody 28C5 heavy chain.
 KW CD14 receptor; monoclonal antibody; 28C5; hybridoma;
 KW antiseptic; therapeutic; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT mat peptide 1..639
 FT /*tag= a
 PN W09428025-A.
 PD 08-DEC-1994.
 PF 27-MAY-1994; U05898.
 PR 28-MAY-1993; US-070160.
 PA (SCRI) SCRIPES RES INST.

PI Leturcq DJ, Mathison JC, Moriarty AM, Tobias PS;

PI Ulevitch RJ;

DR WPI; 95-022719/03.

DR P-PSDB; R64201.

PT Hybridoma cell lines produce MAB which inhibit CD14-mediated cell activation - for detecting CD14 in a sample and to inhibit the binding of LPS to CD14.

PS Disclosure; Fig 2; 91pp; English.

CC Anti-human soluble CD14 receptor MAB 28C5 may be used to

CC detect CD14 in cell samples, to inhibit binding of LPS to

CC CD14 or a LPS/CD14 complex to a cell, to inhibit CD14-mediated

CC activation of a cell expressing CD14 receptor, and for sepsis

CC therapy.

SQ Sequence 639 BP; 144 A; 208 C; 146 G; 141 T;

Query Match 61.6%; Score 253; DB 13; Length 639;

Best Local Similarity 94.1%; Pred. No. 4.39e-156;

Matches 270; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Db 11 agcttcagcagtcaggacccctggcctgtgaacctctcagtcctgtccctcaactgca 70

Qy 62 AGCTTAGGAGTCGGGACCTGCTGGTGAAGCCTTCAGTCTGTGCTCCCTCACCTGCA 121

Db 71 ctgtcactggctactcaatcacagtgattctgctggaactggatcgccgagtttccag 130

Qy 122 CTGTCACTGGCTACTCAATCACAGATGATGCTGGAGCTGATGCTGGAGTTCGAG 181

Db 131 gaacagactggagtgatgggtacataagctacagtgagtgagcactagctacaacctca 190

Qy 182 GAAACAACTGGAGTGGTGGCTACATAAGTTACAGTGGTATCACTACCTACACCCAT 241

Db 191 ctctcaaaagtcgaatctctactcagcagacacatccaaagaccagttctcttcgcagt 250

Qy 242 CTCTCAAAAGTCGATCTATCACTCGACACATCCAGAACCCAGTCTTCTTCACGT 301

Db 251 tgaattcggtgactactgagggacagccacatattactgtgaaga 297

Qy 302 TGAATTCTGTGACTACTGGGGACAGCTCCACATATTACTGTGCAAGA 348

RESULT 6

ID Q66698 standard; DNA; 836 BP.

AC Q66698;

DT 21-DEC-1994 (first entry)

DE Sequence of the single chain antibody gene (scFv) against the haptan

DE dinitrophenol (anti-DNP-scFv).

KW Retroviral vector; antigen binding site; antibody; envelope protein;

KW dinitrophenol; DNP; ss.

OS Synthetic.

PN W09412626-A.

PD 09-JUN-1994.

PF 18-NOV-1993; U11258.

PR 20-NOV-1992; US-979619.

PA (OYNE-) UNIV NEW JERSEY.

PI Dornburg RC;

DR WPI; 94-200255/24.

PT Retroviral vector with target cell specificity - used for gene

PT therapy by direct injection into a patients bloodstream

PS Example; Fig 3; 23pp; English.

CC The genes coding for the heavy and light chain of an antibody

CC against DNP were provided by Dr Ogawa of Scripps Clinic, La Jolla,

CC Ca. The genes were sequenced and published (Riley et al. 1986).

CC Using PCR a single chain antibody gene was constructed using the

CC signal peptide against DNP. The PCR product was cloned into the SmaI

CC site of pBluescript. DNA sequencing confirmed the successful
CC combination of the two gene segments coding for the variable regions
CC of the antigen binding peptide. The complete sequence of the anti-
CC DNP scFv gene is given in Q66698.

SQ Sequence 836 BP; 218 A; 198 C; 213 G; 207 T;

Query Match 61.6%; Score 253; DB 11; Length 836;

Best Local Similarity 84.4%; Pred. No. 4.39e-156;

Matches 347; Conservative 0; Mismatches 58; Indels 6; Gaps 3;

Db 43 atatggtgttaagtctctgtacctgttgacagccctccgggtatctctgtcagaggtg 102

Qy 1 ATGAGAGTGTGATTTCTTTTGGCTGTTACAGCCTTCTCGTATCTCTGTCTGATGTG 60

Db 103 cagcttcaggagtcaggacctagctcgtgaaacctctctgtacctgtcctcaactgt 162

Qy 61 CAGCTTCAGGAGTCGGGACCTGCTCTGGTGAAGCCTTCTCAGTCTCTGTCCCTCACCTGC 120

Db 163 tctgtcactggcgaactccaccagtggtta---ctggaaactggatccggaaattccca 219

Qy 121 ACTGTCACTGGCTACTCAATCACAGTCAATGATGCTGAGTGGATCGGCGAGTTTCCA 180

Db 220 gggattcaacttgagtacatgggtgtacataagctacagtggtgagctactactacaatcca 279

Qy 181 GGAACAACTGGAGTGGATGGGCTACATAAGTTACAGTGGTATCACTACTACACACCA 240

Db 280 tctctcaaaagtccaatctccatcactcgaacacatccaaagaccagtaactactgcag 339

Qy 241 TCTCTAAAGTCGAATCTCTATCACTCGACACACATCCAAGAACCCAGTCTTCTCTACAG 300

Db 340 ttgaattctgtgactactgagggacagccacatattactgtgcaagatatggtggtta-- 397

Qy 301 TTGAATTCTGTGACTACTGGGGACAGTCCACATATTACTGTGCAAGATCCCTAGCTCGG 360

Db 398 actatg-ctatggagtgactgggtcaaggaacctcagtcaccgtctctctca 447

Qy 361 ACTACGGCTATGGACTACTGGGGTCAAGGACCTCAGTCCCGTCTCTCTCA 411

RESULT 7

ID Q06214 standard; DNA; 351 BP.

AC Q06214;

DT 22-JAN-1991 (first entry)

DE VH domain of antibody B against tumour-associated antigens.

KW Tumour-associated antigen; murine monoclonal antibody B;

KW gastrointestinal carcinoma; ovary; pulmonary adenocarcinoma;

KW diagnosis; ss.

OS Mus musculus.

PN EP-388914-A.

PD 26-SEP-1990.

PF 21-MAR-1990; 105322.

PR 24-MAR-1989; DE-909799.

PA (BEHW) BEHRINGERHEKE AG.

PI Bosslet K, Seemann G, Sedlacek HH;

DR WPI; 90-291873/39.

DR P-PSDB; R07318.

PT Monoclonal antibodies to tumour associated antigens - used for

PT diagnosis of malignant tumours etc.

PS Disclosure; Page 12; 18pp; German.

CC Antibody B is produced as described in EP-141079 and binds to cells

CC almost all gastrointestinal carcinomas and to certain ovary

CC carcinomas and pulmonary adenocarcinomas.

CC They are useful in tumour diagnosis and therapy.

CC See also Q06215 for VK of MAB B, Q07312-13 for MAB A and Q06227-30

CC	for MAb C and D.
SQ	Sequence 351 B

Query Match 57.2%; Score 235; DB 1; Length 351;
Best Local Similarity 91.2%; pred. No. 2.41e-143;
Matches 260; Conservative 0; Mismatches 25; Indels

Db

1 ctgcaggagtcaggacctgacctggtgaaaccttctcagtcactttcactcacctgacct 60
||| ||||||| ||||||| ||||||| ||||||| ||| ||||||| ||| ||||||| ||| |||

Qv

64 cttcassagtcgggacctgtcctgggaagcccttcagtcctgtgccctcacttgacct 123

Db 61 gtcaactggctactccatcaccagtggttatagctggcaactggatccggcagtttccagga 120

Qv 124 gtcaactggctactcgaatcacagtgatcatgctgctgacgtgcatccggcagtttccagga 183

Db 121 aacaactgaatggatgggtacatacagtagtggtatacctaactaacacctct 180
|||||
Ov 184 AACAAATCGACTCGCTCCGCTACATACTTACACATCCCTATTCATCTACCTACACCCATCT 243

D_b 181 ctcaaaagtogaatcttatcactcgagacatccaagaaccagttcttcttcgagttg 240
|||||
|||
244 ctcacaaaaccccccaccccccccccccccccccccccccccccccccccccccc
:::

[illegible]

RESULT 8

AC Q30714;
DT 20-MAR-1993 (first entry)
DE Sequence of PCR product linking the Fd sequence with the

DE sequence
KW Filamentous phage; coat protein membrane anchor domain; ss.
OS Synthetic.

PD 29-OCT-1992.
PF 10-APR-1992; U03091.
PR 10-APR-1991; US-683602.

PA (SRI) SCRIPPS RES INST.
PI Barbas C, Kang A, Lerner RA;
DR WPI; 92-382106/46.

antibody, in its coat protein, useful for diagnostic assay, also new phage DNA libraries and mutagenic oligo:nucleotide primers Example: Page 196; 229pp; English.

the example concerns the preparation of a DNA segment encoding a portion of the fusion protein Fd-cpVIII. Fd comprises the VH and CH1 chains. cpVIII is a filamentous phage coat protein membrane anchor domain. Q30714 is the sequence of the PCR product linking the

rd sequence with the cpviii sequence in frame in a 3' to 5' direction. The Fd-cpviii fusion product was then used in directional ligations for the construction of a pCBAK8-2b dicistronic phagemid expression vector.

SQL sequence	830 BF;	196 A;	240 C;	194 G;	200 I;
Query Match	52.8%;	Score 217;	DB 5;	Length 830;	
Best Local Similarity	82.8%;	Prod No. 1	230-130;		

Matches 293; conservative 0; mismatches 36; indels 3; gaps 3
Db 3 gtccagcttctcagtgctggaactggcctggtgaaacctctcagtcgtctctcacc 62

58 GTGCGACTTCAGGAGTCCGCGACCTGTCTCCTGTGTGAAGCCCTCTCACTCTCTCCCTCACC 117

Db 63 tgctctgtcactgactactccatcaccagtgcattattactgggaactggatccggcagttt 122
||| |||||||| |||||| |||||||| | |||| |||||||| |||||
Ow 118 TGCACGTGTCAGTGGTGACTCAATCACCAGTCATCATGCCCTGGCAGCTGGATCCGGCAGTTT 177

Db 123 ccaggaaacaaactggaatggatggctacataagctacgacgtgtcaataagtatgat 182
|||||
Ov 178 CCAGGAAACAAACTGGAATGGCTACATAAGTACACTGGTATCACTACCCTACAAC 237
|||||

Db 183 ccattctcagaatcgaaatctccatcacctcgtgacacatctaacaatcagtttttcag 242
||||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
Ov 238 CCATCTCTCAAAAGTCGAATTCTTATCATCTCCGACACACATCCAAGAACCACCTCTTCTTA 297

[illegible][illegible]

RESULT 9

AC	Q30706;
DT	20-MAR-1993 (first entry)
DE	Sequence of Clone 21b expressing variable heavy (VH) and constant

KW Nitrophenylphosphonamide; NPN; ligand; receptor binding;
immunoglobulin; light chain; heavy chain; ss.
OS Synthetic.

PD 29-OCT-1992.
PF 10-APR-1992; U03091.
PR 10-APR-1991; US-683602.

PA (SCRI) SCRIPPS RES INST.
PI Barbas C, Kang A, Lerner RA;
DR WPI; 92-382106/46.

PT antibody, in its coat protein, useful for diagnostic assay, also
PT new phage DNA libraries and mutagenic oligo:nucleotide primers
PS Example; Page 188; 229pp; English.

CC expressing the heavy (Fd consisting of VH and CH1) and light (kappa) chains (VL, CL) of antibodies targeted to the periplasm of *E. coli* for the assembly of heterodimeric Fab molecules. The DNA

homologues were prep. and inserted into a *bla* expression vector.
 VH and VL DNA homologues were then randomly combined on the same
 expression vector. Anti-nitrophenylphosphonamide (NPN) reactive
 heterodimer-producing dicistronic vectors were then selected.

CC clone 2b is one of the plaques which reacted with rFN. The sequence
CC of clone 2b Fd chain is given in Q30706. The sequence of the kappa
CC light chain variable and constant regions are given in Q30707 and
CC Q30708 respectively.

SQ sequence 798 BF; 190 A; 239 C; 179 G; 190 I;
 Query Match 51.8%; Score 213; DB 5; Length 798;
 Best Local Similarity 92.2%; Prod No. 9 10a-12b;

Matches 291; Conservative 0; Mismatches 60; Indels 3; Gaps 0

Db 103 gtgaaactgctcgagtcaggaaactggcctcgtgaaaccttcagtcgtctgtctcacc 162

QY	58	GTGAGCTTCAGAGTGGCGGAGCTGTCTGTGTGAAGCGCTTCAGTCTCTGTGCTCCATCC	117
Db	163	Tgctctgtcactgactactccatccacagtcttattactggaactggatccgcagattt	222
QY	118	TGCATCTGTCACTGGCTACTCAATACCACTGATCATGCGCTGAGCTGGATCCGGACGTTT	177
Db	223	ccagaaacaaactggaatggaatggctgacctacataagctacgacgctgtccaataaagtatgat	282
QY	178	CCAGAAACAAACTGGAGTGATGGGCTACATAATAGTTACAGTGGTATCTACTTACCTAACAC	237
Db	283	ccatctctcaagaatcgaatctccatcactcgtgacacatctcaaatcagttttccag	342
QY	238	CCATCTCTCAAAATCGCAATCTCTATCACTCGAGACACATCCAAAGACCAGTCTTCTCTA	297
Db	343	aadtgatttctgtcattcttgaggacacaggaaacataatgactgttccaaggagg--a-ct	399
QY	298	CAGTTGAAATTTCTGTACTCTGCGGACAGCTCCACATATTACTGTGCAAGATCCCTAGCT	357
Db	400	agggctctgctatggaactactggggtcaaggaaatttcagtcacccgtctctctca	453
QY	358	CGGACTACGGGTATGAGTACTGTGGGTCAAGAACTCTAGTCCGCTTCTCTCA	411

RESULT	10	
ID	Q44642 standard; DNA; 798 BP.	
AC	Q44642;	
DT	04-OCT-1994 (first entry)	
DE	Fd phage clone sequence comprising kappa light chain regions.	
KW	Expression; kappa light chain; antibody; expression vector;	
KW	bacteriophage; clone; Fd; ds.	
OS	Synthetic.	
PN	W09405781-A.	
PD	17-MAR-1994.	
PF	03-SEP-1993; U08364.	
PR	04-SEP-1992; US-941369.	
PA	(SCRI) SCRIPPS RES INST.	
PI	Lerner RA, Light JP;	
DR	WPI; 94-101186/12.	
PT	Filamentous phage comprising a heterologous polypeptide and a	
PT	hetero:dimer - is used to detect the presence of a preselected	
PT	ligand in a sample	
PS	Example 2f; Page 198; 232pp; English.	
CC	This synthetic sequence was packaged into the filamentous phage Fd.	
CC	It comprises kappa light chain variable and constant regions. The	
CC	clone encodes anti-NPN (Nitrophenylphosphonamide) reactive	
CC	heterodimers.	
SQ	Sequence 798 BP; 190 A; 238 C; 179 G; 191 T;	
Query Match	51.8%; Score 213; DB 10; Length 798;	
Best Local Similarity	82.4%; Pred. No. 8.10e-128;	
Matches	291; Conservative 0; Mismatches 60; Indels 3;	

Db	103	gtgaactgtctcagtcagagctcgtcctcgtgaaacctctcagtcctctgtctctcacc	162
Qy	58	gtcagcttccagagatcgaggacatgtcctcgtggaagccttctcagctctgtctcctcacc	117
Db	163	tgctctgtcactgaactactccatcaccagtgcttattactggaactggatccggcagttt	222
Qy	118	tgcactgtctcactgcgtactcaatcacacagtgatcatgccttgagctgcatcggcagcttt	177
Db	223	ccaggaaacaactggaatggatgggctacataagctacgacggtgtcacaatgaatttat	282
Qy	178	ccaggaaacaacttggngtgatgggtcattatgattacagtggttctcactacctcaaac	237

Db	283	ccatctctcaagaatcgaatctccatctactcgtgacacatctacaatatcagtttttcag	342
QY	238	CCATCTCTCAAAAGCGAATCTCTATCACTCGAGACACATCCAGAACCAGTTCCTCTTA	297
Db	343	aadtgattcttgactctcgaggacacaggaacatatgactgttcaagagg--a-ct	399
QY	298	CAGTTGAAATCTTGCTACTGCGGGACAGTCCACATATTACTGTGCAAGATCCCTAGCT	357
Db	400	agggacctgctatggaactactgggggtcaagggaatttcagtcacccgtctccctca	453
QY	358	CGGACATCCGGGTATGCACTACTGGGTTCAGGAACCTCTAGTCCCGTCTCTCTCA	411

RESULT	11
ID	Q31365 standard; DNA; 438 BP.
AC	Q31365;
DT	30-MAR-1993 (first entry)
DE	pUC-RVH-PW1f-4.
KW	Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR;
KW	complementarity determining region; mouse; monoclonal; hybridoma;
KW	plasmid; polymerase chain reaction; amplify; <i>es</i> .
OS	Synthetic.

RESULT 11

ID	Q31365	standard; DNA; 438 BP.
AC	Q31365;	
DT	30-MAR-1993	(first entry)
DE	PUC-RVH-PM1f-4.	
KW	Human; antibody; interleukin-6; receptor; IL-6R; CD8; PCR;	
KW	complementarity determining region; mouse; monoclonal; hybridoma;	
KW	plasmid; polymerase chain reaction; amplifi; ss.	
OS	Synthetic.	
FX		
Key	Location/Qualifiers	
FT	CD5	12..425
FT	/*tag= a	
FT	sig_peptide	12..68
FT	/*tag= b	
FT	mat_peptide	69..425
FT	/*tag= c	
FT	WO9219759-A.	
PN	PD 12-NOV-1992..	
PF	24-APR-1992; J00544.	
PR	25-APR-1991; JP-095476.	
PR	19-FEB-1992; JP-032084.	
PA	(CHUS) CHUGAI SEIYAKU KK.	
PI	Bendig MW, Jones ST, Saldanha JW, Sato K, Tsuchiya M;	
DR	WPI; 92-398882/48.	
DR	P-PSDB; R29014.	
PT	Reconstituted human antibody to human interleukin-6 receptor -	
PT	has low antigenicity and contains mouse V-region complementarity	
PT	determining regions	
PS	PTC Disclosure; Page 142-3; 207pp; Japanese.	
CC	The sequences given in Q31360-61 and Q31365-66 are plasmids encoding	
CC	portions of monoclonal antibodies which were derived from mouse	
CC	hybridomas. The DNA encoding complementarity determining regions	
CC	(CDR's) was isolated by polymerase chain reaction. The antibodies	
CC	produced recognises human interleukin-6 receptor (IL-6R). The	
CC	hybridoma cells were transformed with plasmids containing fragments	
CC	of the antibody gene which caused the production of the antibody from	
CC	the hybridoma cells.	
SQ	Sequence 438 BP; 105 A; 123 C; 113 G; 97 T;	

	Query Match	40.6%;	Score 167;	DB 5;	Length 438;
	Best Local Similarity	72.6%;	Pred. No. 1.45e-95;		
	Matches	268;	Conservative	0;	Mismatches 101;
					Indels
					0;
					Gaps
					0;
Db	57	ggtgtccaactccaaggtccaactgcagagagcgggtccaggtctttgtgagacctgacag	116		
Qy	43	GGTATCTGTGATGTCAGGCTTCAGAGTCGGAGCTGTCTGGTCAAGCCCTTCTCAG	102		
Db	117	acctgagcctgacctgcacggtgtctggtcactcaattaccagcgatcatgcctggagc	176		
Qy	103	TCCTCTGCTCCATCGCTGCTCATCTGCTACTCAATCACAGTCATGCTGGAGC	162		

Query Match	38.9%;	Score 160;	DB 13;	Length 624;
Best Local Similarity	76.5%;	Pred. No. 1.09e-90;		
Matches 231;	Conservative 0;	Mismatches 71;	Indels 0;	Gaps 0;
Db	282	tctgtcccaggtgcagctgcagagtgctgggcccagagctggtgaagccttcggacacc	341	
Qy	47	TCCTGTCTATGTGCAGCTTCAGAGCTCGGGACCTGCTCGGTGAACCTTCTCAGTC	106	
Db	342	tgtccctcacctgcgtgtctctggttactccatcagcagtagtaactgtgggctgga	401	
Qy	107	TGTCCTTACCTGCAGCTGTCTACTGTCTCAATCAGCATCATCTCGCTGGAGCTGA	166	
Db	402	tccggcagcccccaggaaggagctggagtggatgggtacatctattatagtgaggaca	461	
Qy	167	TCGGCGCAGTTTCAGGAAACAAACTGGAGTGATGGCTACATTAAGTTACGTGGTATCA	226	
Db	462	cctactacaaccogtccctcaagagtcagagtcaccatgtcagtagacagctccaagaacc	521	
Qy	227	CTACCTTACAACCCATCTCTCAAAAGTCGAATCTTATCATCTCGAGACACATCCAGAACC	286	
Db	522	agttctccctgaagctgagctctgtgaccgcgtggacacggccgtgtatctactgtcgga	581	
Qy	287	AGTTTCTCTACAGTTGAATTCGTGACTCTGGGACAGCTGCACATTAATCTGTGCAAC	346	

RESULT	15	
ID	Q42699	standard; DNA; 348 BP.
AC	Q42699;	
DT	01-NOV-1993	(first entry)
DE	VH411.	
KW	Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;	
KW	CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;	
KW	chain; epitope; immune deficiency; <i>ss</i> .	
OS	Homo sapiens.	
Key	Location/Qualifiers	
FT	sig_peptide	1..57
FT	/*tag=	a

Search completed: Mon Jul 8 09:03:06 1996
Job time : 42 secs.

WATERMAN

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 09:03:25 1996; MasPar time 190.43 Seconds

Tabular output not generated. 775.895 Million cell updates/sec

Title: >US-08-137-117B-30

Description: (1-411) from US08137117B.seq

Perfect Score: 411

N.A. Sequence: 1 ATCAGAGTGGTGAATCTTTT.....CCTCAGTCACCGTCTCTCA 411

Comp: TACTCTCACCAGCTAAGAAA.....GGAGTCAGTGGCAGAGAGT

Scoring table:

TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:STS1 90:STS2 91:STS3 92:STS4
93:STS5 94:STS6
EST-STS-TWO
95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5
100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10
105:gnEST11 106:gnEST12 107:gnEST13 108:gnEST14 109:gnEST15
110:gnEST16 111:gnEST17 112:gnEST18 113:gnEST19 114:gnEST20
115:gnEST21 116:gnEST22 117:gnEST23 118:gnEST24 119:gnEST25
120:gnEST26 121:gnEST27 122:gnEST28 123:gnEST29
124:gnEST30 125:gnEST31 126:gnEST32 127:gnEST33

Database:

EST-STS-TWO
95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5
100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10
105:gnEST11 106:gnEST12 107:gnEST13 108:gnEST14 109:gnEST15
110:gnEST16 111:gnEST17 112:gnEST18 113:gnEST19 114:gnEST20
115:gnEST21 116:gnEST22 117:gnEST23 118:gnEST24 119:gnEST25
120:gnEST26 121:gnEST27 122:gnEST28 123:gnEST29
124:gnEST30 125:gnEST31 126:gnEST32 127:gnEST33

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

Statistics: Mean 9.954; Variance 1.799; scale 5.535

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	137	33.3	478	16	H43753	yp21g01.r1 Homo sapie	1.01e-239
2	137	33.3	478	123	HS753236	yp21g01.r1 Homo sapie	1.01e-239
3	103	25.1	299	127	HST27727	EST13874 Homo sapiens	1.08e-164
4	103	25.1	299	69	T27727	EST13874 Homo sapiens	1.08e-164
5	100	24.3	410	13	H30111	yo59b04.r1 Homo sapie	3.57e-158
6	92	22.4	331	69	T27715	EST13381 Homo sapiens	6.72e-141
7	92	22.4	331	127	HST27715	EST13381 Homo sapiens	6.72e-141
8	73	17.8	234	69	T28164	EST30734 Homo sapiens	1.19e-100
9	73	17.8	234	127	HST28164	EST30734 Homo sapiens	1.19e-100
10	63	15.3	180	127	HST27730	EST13989 Homo sapiens	4.58e-80
11	63	15.3	180	69	T27730	EST13989 Homo sapiens	4.58e-80
12	57	13.9	169	47	R48619	y168a01.r1 Homo sapie	5.50e-68
13	41	10.0	367	78	T60021	yc01g07.r1 Homo sapie	3.12e-37
14	39	9.5	325	70	T29716	EST91759 Homo sapiens	1.36e-33
15	39	9.5	325	122	HST71611	EST91759 Homo sapiens	1.36e-33
16	38	9.2	253	70	T29661	EST89449 Homo sapiens	8.53e-32
17	38	9.2	253	122	HS66110	EST89449 Homo sapiens	8.53e-32
18	37	9.0	330	64	SSCID10	S.scrofa mRNA; expres	5.15e-30
19	37	9.0	330	129	SSCID10	S.scrofa mRNA; expres	5.15e-30
20	36	8.8	228	11	H24604	y140b06.r1 Homo sapie	2.99e-28
21	36	8.8	419	124	HS816226	ys11b01.r1 Homo sapie	2.99e-28
22	36	8.8	419	100	H73816	ys11b01.r1 Homo sapie	2.99e-28
23	34	8.3	422	125	HS952232	yo70g05.r1 Homo sapie	8.91e-25
24	34	8.3	422	16	H43952	yo70g05.r1 Homo sapie	8.91e-25
25	31	7.5	125	8	H15753	y127d09.r1 Homo sapie	1.02e-19
26	31	7.5	485	49	R54774	y175f04.r1 Homo sapie	1.02e-19
27	30	7.3	303	57	R83139	y11g003.r1 Homo sapie	4.44e-18
28	29	7.1	446	53	R71741	y185d11.r1 Homo sapie	1.83e-16
29	26	6.3	147	16	H42647	y13a12.r1 Homo sapie	8.57e-12
30	26	6.3	369	10	H22104	y13a12.r1 Homo sapie	8.57e-12
31	26	6.3	418	78	T61697	yb86f08.r1 Homo sapie	8.57e-12
32	25	6.1	309	12	H27953	y162c09.r1 Homo sapie	2.67e-10
33	25	6.1	412	12	H27044	y165f02.r1 Homo sapie	2.67e-10
34	25	6.1	448	17	H46398	y19d12.r1 Homo sapie	2.67e-10
35	24	5.8	48	16	H42610	y13d04.r1 Homo sapie	7.62e-09
36	24	5.8	538	8	H14008	y127b02.r1 Homo sapie	7.62e-09
37	23	5.6	189	89	DM68G8S	D. melanogaster STS d	1.99e-07
38	23	5.6	223	121	HS593219	yu69e06.r1 Homo sapie	1.99e-07
39	23	5.6	223	99	H68593	yu69e06.r1 Homo sapie	1.99e-07
40	22	5.4	236	13	H33938	EST110390 Rattus sp.	4.70e-06
41	22	5.4	236	129	R39382	EST110390 Rattus sp.	4.70e-06
42	22	5.4	355	131	HS45TS735	Human Chromosome 4 (c	4.70e-06
43	22	5.4	355	93	HUM4STS735	Human Chromosome 4 (c	4.70e-06
44	21	5.1	329	10	H22208	y138e08.r1 Homo sapie	9.97e-05
45	21	5.1	408	16	H42300	yo63g08.r1 Homo sapie	9.97e-05

ALIGNMENTS

RESULT LOCUS	1	H43753	478 bp	mRNA	EST	31-JUL-1995
--------------	---	--------	--------	------	-----	-------------

Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@db.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@db.tigr.org).

NCBI gi: 609813
FEATURES
source 1..331
/organism="Homo sapiens"
/note="human"
mRNA <1..>331
BASE COUNT 62 a 90 c 91 g 80 t 8 others
ORIGIN

Query Match 22.4%; Score 92; DB 69; Length 331;
Best Local Similarity 70.0%; Pred. No. 6.72e-141;
Matches 177; Conservative 0; Mismatches 73; Indels 3; Gaps 2;
Db 72 tctgtccagctgcagctgcagagtcggccagagactggtgaaccttcggagacc 131
Qy 47 TCTGTCTGTGTCGATGTCAGGAGTCGGGACCTGTCTGTGTAAGCCTTCAGTCTC 106
Db 132 tgcctccactgcactgtctctgtgtgtntccgtctacagtgacaattttnactggggt 191
Qy 107 TGTCCCTCAGCTGCAGCTGCAGTGGCTACTCAATCACCAGTGATCATG--C-CTGGAGCT 163
Db 192 ggggtccagccagccaggaagggtggagtgattgggactattttnatagtgga 251
Qy 164 GGATCCGGGAGTTTCAGGAAACAACTGGAGTGGGCTTACATGATGATGATGATGATG 223
Db 252 caactactacaaacngtcctcaggagtcgagtcaccatcttcgtagcangtcagaa 311
Qy 224 TCATCTACCTACACCCATCTCTCAAAAGTCGAATCTCTATCTACCTCGAGACATCCAGA 283
Db 312 acaagttctccct 324
Qy 284 ACCAGTTCTTCT 296

RESULT 7
ID HST27715 standard; RNA; EST; 331 BP.
AC T27715;
DT 12-JAN-1995 (Rel. 42, Created)
DT 07-SEP-1995 (Rel. 45, Last updated, Version 2)
DE EST13381 Homo sapiens cDNA 5' end similar to immunoglobulin gamma
DE heavy chain V region (GB:M97921) (Ht:3789).
KW EST.

OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.
RN [1]
RP 1-331
RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
RA Bult C.J., Lee N., Kirkness E.F., Weinstein K.G., Gocayne J.D.,
RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
RA Fitzgerald L.M., Fitzhugh W.M., Fritchman J.L., Geoghagen N.S.M.,
RA Glodex A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,
RA Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,
RA Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
RA Meisener P.S., Olsen H., Raymond L., Wei Y.F., Wang J., Xu C.,
RA Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;
RT *Initial Assessment of Human Gene Diversity and Expression
RT Patterns Based Upon 52 Million Basepairs of cDNA Sequence*;
RL Unpublished.
CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper
CC Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:
CC tdbinfo@db.tigr.org For clone availability, additional sequence
CC and expression information related to this EST, please contact the
CC TIGR Database (tdbinfo@db.tigr.org). NCBI gi: 609813
FH Key Location/Qualifiers
FT source 1..331
FT /organism="Homo sapiens"
FT /note="human"
FT mRNA <1..>331
SQ Sequence 331 BP; 62 A; 90 C; 91 G; 80 T; 8 other;

Query Match 22.4%; Score 92; DB 127; Length 331;
Best Local Similarity 70.0%; Pred. No. 6.72e-141;
Matches 177; Conservative 0; Mismatches 73; Indels 3; Gaps 2;
Db 72 tctgtccagctgcagctgcagagtcggccagagactggtgaaccttcggagacc 131
Qy 47 TCTGTCTGTGTCGATGTCAGGAGTCGGGACCTGTCTGTGTAAGCCTTCAGTCTC 106
Db 132 tgcctccactgcactgtctctgtgtntccgtctacagtgacaattttnactggggt 191
Qy 107 TGTCCCTCAGCTGCAGCTGCAGTGGCTACTCAATCACCAGTGATCATG--C-CTGGAGCT 163
Db 192 ggggtccagccagccaggaagggtggagtgattgggactattttnatagtgga 251
Qy 164 GGATCCGGGAGTTTCAGGAAACAACTGGAGTGGGCTTACATGATGATGATGATGATG 223
Db 252 caactactacaaacngtcctcaggagtcgagtcaccatcttcgtagcangtcagaa 311
Qy 224 TCATCTACCTACACCCATCTCTCAAAAGTCGAATCTCTATCTACCTCGAGACATCCAGA 283
Db 312 acaagttctccct 324
Qy 284 ACCAGTTCTTCT 296

RESULT 8
LOCUS T28164 234 bp mRNA EST 06-SEP-1995
DEFINITION EST30734 Homo sapiens cDNA 5' end similar to immunoglobulin heavy
chain V,D,J regions (GB:214206) (Ht:3118).
T28164
ACCESSION
KEYWORDS EST.
SOURCE human primer=M13 Reverse library=Human Colon.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 234)

AUTHORS

Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Klinek K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A., Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Meissner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C., Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M. and Venter J.C.

TITLE
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

JOURNAL

COMMENT

Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).

NCBI gi: 610262

FEATURES
Location/Qualifiers
source
1..234

/organism="Homo sapiens"
/note="human"

mRNA
<1..>234

BASE COUNT
ORIGIN
41 a 63 c 72 g 52 t 6 others

Query Match 17.8%; Score 73; DB 69; Length 234;

Best Local Similarity 74.3%; Pred. No. 1.19e-100;

Matches 104; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db 72 tctgtgccaggtgcagctgcaggagtcgggncagngctggtgacgttttnggagacc 131

||||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||

Qy 47 TCCTGTCTGATGTCGACCTTCAGGAGTCGGGACCTGCTCTGTGTCGACCTTCAGTC 106

Db 132 tgcctccacctgngctgtctgtgttactccataagaagtgttactactgggctgga 191

||||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||

Qy 107 TGTCCCTCACCCTGCACCTGTGCTACTGCTACTCAATCACCAGTGTATGCTGGAGCTGGA 166

Db 192 ttcggcangccagggaac 211

||||| | ||||| | ||

Qy 167 TCCGGCAGTTTCCAGGAAC 186

RESULT

ID HST28164 standard; RNA; EST; 234 BP.

AC T28164;

DT 12-JAN-1995 (Rel. 42, Created)

DE EST30734 Homo sapiens cDNA 5' end similar to immunoglobulin heavy

chain V, D, J regions (GB:214206) (HT:3118).

KW

EST

OS Homo sapiens (human)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
RP 1-234
RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
RA Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,
RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W.,
RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
RA Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,
RA Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,
RA Kelley J.M., Klinek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,
RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,
RA Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M.,
RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
RA Meissner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C.,
RA Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;
RT *Initial Assessment of Human Gene Diversity and Expression
Patterns Based Upon 52 Million Basepairs of cDNA Sequence*;
RL Unpublished.
CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper
Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:
CC tdbinfo@tdb.tigr.org For clone availability, additional sequence
and expression information related to this EST, please contact the
CC TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 610262

FH Key Location/Qualifiers

FT source
1..234
/organism="Homo sapiens"

FT mRNA
<1..>234

FT SQ Sequence 234 BP; 41 A; 63 C; 72 G; 52 T; 6 other;

Query Match 17.8%; Score 73; DB 127; Length 234;

Best Local Similarity 74.3%; Pred. No. 1.19e-100;

Matches 104; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Db 72 tctgtgccaggtgcagctgcaggagtcgggncagngctggtgacgttttnggagacc 131

||||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||

Qy 47 TCCTGTCTGATGTCGACCTTCAGGAGTCGGGACCTGCTCTGTGTCGACCTTCAGTC 106

Db 132 tgcctccacctgngctgtctgtgttactccataagaagtgttactactgggctgga 191

||||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||

Qy 107 TGTCCCTCACCCTGCACCTGTGCTACTGCTACTCAATCACCAGTGTATGCTGGAGCTGGA 166

Db 192 ttcggcangccagggaac 211

||||| | ||||| | ||

Qy 167 TCCGGCAGTTTCCAGGAAC 186

RESULT

ID HST27730 standard; RNA; EST; 180 BP.

AC T27730;

DT 12-JAN-1995 (Rel. 42, Created)

DE EST13989 Homo sapiens cDNA 5' end similar to immunoglobulin heavy

chain, V region (GB:212364) (HT:3115).

KW EST.

DE EST91759 Homo sapiens cDNA 5' end similar to immunoglobulin heavy
DE chain V.D.J regions (GB:M34029) (HT:3782).

Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea; Hominidae.
RN [1]

RA Kelley J.M., Klimak K.M., Kelley J.C., Liu L.I., Marmaros S.M.,
RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,
RA Fischer C., Haestings G.A., He W.W., Hu J.S., Greene J.M.,
RA Gruber J., Hudson P., Kim A., Korzak D.L., Kunsch C., Ji H., Li H.,
RA Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wang J., Xu C.,

RA Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;
RT "Initial Assessment of Human Gene Diversity and Expression
RT Patterns Based Upon 52 Million Basepairs of cDNA Sequence";
RL Unpublished.

RL Unpublished
 CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper
 CC Rd, Gaithersburg, MD 20878 Tel: 3019699056 Fax: 3019699423 Email:
 CC tdbinfo@db.tigr.org For clone availability, additional sequence
 CC and expression information related to this EST, please contact the
 CC TIGR Database (tdbinfo@db.tigr.org) . NCBI gi: 611814
 FH Key Location/Qualifiers

```

FT      /note="human"
SQ      mRNA
SQ      Sequence 325 BP, 72 A; 92 C; 81 G; 80 T; 0 other;
        <1..>325
Query Match      Score 39; DB 122; Length 325;
Best Local Similarity 75.3%; Pred. No. 1.36e-33;
Matches 58; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```

Qy	43	GGTATCTGCTGATCGACGTTTCAGGATCGGGACCTCTCTGGTAGCGTTCTCTAG	102
Db	148	accctctcaetcaactg	164
Qy	103	TTCTGTGCGCTCACTG	119

Search completed: Mon Jul 8 09:06:44 1996
Job time : 199 secs.

RESULT 15

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	393	100.0	393	5	Q30753		p12-k2.	2.00e-242
2	344	87.5	417	16	Q90432		DNA encoding anti-idi	3.41e-209
3	331	84.2	438	16	Q90431		DNA encoding anti-idi	2.15e-200
4	303	77.1	396	14	Q83490		Mouse MAb 3B9 light c	1.81e-181
5	303	77.1	393	16	Q92501		Mouse antibody FB3-2	1.81e-181
6	309	76.1	723	16	Q92503		Mouse antibody FB4-7	9.06e-179
7	297	75.6	336	16	Q98534		Vl coding sequence fr	2.03e-177
8	295	75.1	393	6	Q36609		Anti-CD4 antibody MT	4.53e-176
9	293	74.6	393	5	Q30757		p64-k4.	1.01e-174

RESULT	1
ID	Q30753 standard; cDNA; 393 BP.
AC	Q30753;
DT	30-MAR-1993 (first entry)
DE	p12-k2.
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;
KW	plasmid; p12-k2; p12-h2; ss.

PT has low antigenicity and contains mouse V-region complementarity determining regions
PT Disclosure: Page 118; 207pp; Japanese.
PS The sequences given in Q30753-34 were used in example to illustrate
CC the production of a human antibody which recognises human
CC interleukin-6 receptor (IL-6R). The antibody comprises light (L)
CC chain and heavy (H) chain variable regions which were derived from a
CC mouse monoclonal antibody produced from the hybridoma AUK12-20 which
CC contained the plasmids p12-k2 and p12-h2.
SQ Sequence 333 BP; 98 A; 103 C; 103 G; 89 T;

Query Match	100.0%	Score 393;	DB 5;	Length 393;
Best Local Similarity	100.0%;	Pred. No. 2.00e-242;		
Matches	393;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;

Db	1	atggagtcagacacacctcctgctatdgggtactgctctgggttcagagttccactggt	60
Qy	1	ATGGAGTCAGACACACTCCTGCTATGGGTACTGCTCTGGGTTCCAGGTTCCACTGGT	60
Db	61	gacattgtgtgacacagctcctgttcttccttagtgtatctctggggcagagggccacc	120
Qy	61	GACATTGTGTGACAGACTCTCTGCTTCTTGGTGTATCTCTGGGGCAGAGGGCCACC	120
Db	121	atctcatgcaggggccagcaaaagtgcagtacatctggctatagtatatagcactggtac	180
Qy	121	ATCTCATGCAGGGGCCAGCAAAAGTGTCAGTACATCTGGCTATAGTTATATGCACTGGTAC	180
Db	181	caacagaaacaggcagacagaccacaaactcctcatctatcttgatccaactagaatct	240
Qy	181	CAACAGAAACAGGACAGACAGACCACAAACTCCTCATCTATCTTTGCATCCAACCTAGAAATCT	240
Db	241	ggggtcctgccaggttcagtggcagtggggtctgggacagacttcacccccaacatccat	300
Qy	241	GGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT	300
Db	301	cctgtggagaggaggatgctgcaacctattactgtcagcacagtagggagaatccgtac	360
Qy	301	CCTGTGGAGAGGAGGAGTCTGCTCAACCTATTACTGTCAGCACAGTAGGGAGAAATCCGTAC	360
Db	361	acgttcggaggggggacgaagctggaaaataaaaa	393
Qy	361	ACGTTCCGAGGGGGGACCAAGCTGGAATAAAAA	393

RESULT	2
ID	Q90432 standard; DNA; 417 BP.
AC	Q90432;
DT	02-FEB-1996 (first entry)
DE	DE DNA encoding anti-idiotypic antibody Tld20 clone 20Kb1.
DE	Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW	complementarity determining region; ds.

File	Key	Location/Qualifiers
FD	CDS	28..417
FT	/*tag= a	
FT	/product= anti-autoantibody_idio20	
FT	/sig_peptide	28..90
FT	/*tag= b	
PD	J0710199-A.	
PN	18-APR-1995.	
PF	06-OCT-1993;	272950.
PF	06-OCT-1993;	JP-272950.
PA	(HAGI/) HAGIWARA Y.	
DR	WPI; 95-192987/24.	

DR	P-PSDB; R74967.
PT	Novel anti-idiotype antibody against an human anticancer monoclonal
PT	antibody - and DNA sequences encoding the antibody, useful in
PT	pharmacology, medicine and biochemical fields.
PS	Example 5; Page 20; 28pp; Japanese.
CC	Q90425-090434 are DNA clones encoding anti-idiotype antibodies
CC	Id30, Id107, Id120, Id33 against a human anticancer
CC	monoclonal antibody. These antibodies and DNA encoding them are useful
CC	in pharmacological, medical and biochemical fields of research.
SQ	sequence 417 BP; 100 A; 110 C; 113 G; 94 T;

Query Match 87.5%; Score 344; DB 16; Length 417;
Best Local Similarity 95.7%; Pred. No. 3.41e-209;
Matches 376; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

Db	28	atggagacagacacactcctgctatgggtacgtcgtctcgggtccagggtccactcgggt	87
Qy	1	ATGGAGTTCAGACACACTCTCGTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGT	60
Db	88	gacattgtctgcacacagtcctctgcttcttagctgtatctctggggcagagggccacc	147
Qy	61	GACATTGTCTGTCACAGTCTCTGCTCTCTTAGTGGTGATCTCTGGGGCAGAGGGCCACC	120
Db	148	atctcatacaggggccagcaaaagtgtcagtacatctggctatagttatatatgcactggaac	207
Qy	121	ATCTCATCGAGGGCCAGCAAAAGTGTGAGTCTGGCTATGCTATATGCACTGGGTAC	180
Db	208	caacagagacaggagacagcaccacagctcctcatctcttgtatccaaacctagaactct	267
Qy	181	CAACAGAAACAGGACAGACAGACCCAACTCCTCATCTATCTTTGCATCCAACTCAGAATCT	240
Db	268	gggggtccctgccaggttcagtgggcagtggggtcgtgggacagacttcacctcaactccat	327
Qy	241	GGGGTCCCTGCCAGGTTGAGTGGCAGTGGGCTCGGACAGACTTCACCCCTCAACATCCAT	300
Db	328	ccctgtgagagagagagatgtcgcaacctattactgtcagcacattgagg--cttac	384
Qy	301	CCGTGTGGAGGAGGAGATGCTGCAACCTTACTGTCTCAGCACAGTAGGGAGAAATCCGTAC	360
Db	385	acgttcggaggggggacaaagctggaaataaaa	417
Qy	361	ACGTTGCGAGGGGGACCAAGCTGGAATAAAA	393

RESULT	3
ID	Q90431 standard; DNA; 438 BP.
AC	
DC	02-FEB-1996 (first entry)
DE	DNA encoding anti-idiotypic antibody
DT	Idiol7 clone 17KBL.
DI	Antibody; cancer; CDR; heavy chain;
KE	light chain; immunoglobulin;
KW	complementarity determining region, ds.

PH	Key	Location/Qualifiers
FT	CDS	1..438
FT	/*tag= a	
FT	/product= anti-idiotypic_antibody_Idiol17	
FT	sig_peptide	1..39
FT	/*tag= b	
PN	J07101999-A.	
PD	18-APR-1995.	
PR	06-OCT-1993; 272950.	
PR	06-OCT-1993; JP-272950.	
PA	(HAGI)/ HAGIWARA Y.	
DR	WPI; 95-182987/24.	

DR P-PSDB; R74966.
PT Novel anti-idiotypic antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
PS Example 5; Page 19; 28pp; Japanese.
CC Q90425-Q90434 are DNA molecules encoding anti-idiotypic antibodies
CC Idio3, Idio17, Idio20, Idio27 and Idio33 against a human anticancer
CC monoclonal antibody. These antibodies and DNA encoding them are useful
CC in pharmacological, medical and biochemical fields of research.
SQ Sequence 438 BP; 104 A; 120 C; 112 G; 102 T;

Query Match 84.2%; Score 331; DB 16; Length 438;
Best Local Similarity 96.5%; Pred. No. 2.15e-200;
Matches 359; Conservative 0; Mismatches 10; Indels 3; Gaps 2;

Db 1 ctatgggtactgtctgtgggtccaggttccactggtgacattgtgtgacacagtct 60
|||||
Qy 22 CTATGGGTACTGCTGCTGGGTTCAGTTCCACTGCTGACATTGCTGCACAGTCT 81
|||||
Db 61 cctgtcttcctagctgtatctctggggcagagggtccctccatctcatcacagggccagcaaa 120
|||||
Qy 82 CTGTCTTCCTTAGGTGTATCTCTGGGCAGAGGGCCACCATCTCATGCGAGGGCCAGCAAA 141
|||||
Db 121 agtgcagtcacatctggctatgtatgtacactggaaccaacagacagagacgcca 180
|||||
Qy 142 AGTGTCACTACATCTGGCTATGTTATATGCACTTGTATGCAACAGAAACCGACAGACA 201
|||||
Db 181 cccaactcctcatctatcttggatccaaactagaatctgggtccctgccaggttcagt 240
|||||
Qy 202 CCMAACTCCTCATCTATCTTGATCCAACTAGAACTCGGGTCCCTCCAGGTTTCAGT 261
|||||
Db 241 ggcagtgggtctggacagactccacctcaacatccatccctgtggaggaggaggtgct 300
|||||
Qy 262 GGCAGTGGGTCTGGACAGACTTCACCTCAATCCATCTCTGTGGAGGAGGAGTGC 321
|||||
Db 301 gcaacctattactgtcagcacattagg--gag--cttacagttcggagggggagcaag 357
|||||
Qy 322 GCACCTATTACTGTCACACAGTACGAGAGATCCGTACAGTTCGAGGGGGGACCAAG 381
|||||
Db 358 ctggaaataaaa 369
|||||
Qy 382 CTGGAATAAAA 393
|||||

RESULT 4
ID Q83490 standard; cDNA; 396 BP.
AC Q83490;
DT 20-SEP-1995 (first entry)
DE Mouse MAb 3B9 light chain.
KW Chimeric antibody; humanized antibody; antibody engineering;
KW monoclonal antibody; MAb; interleukin-4; IL-4; allergy; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 1..396
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
FT mat_peptide 61..396
FT /*tag= c
FN W09507301-A.
PD 16-MAR-1995.
PF 07-SEP-1994; U10308.
PR 07-SEP-1993; US-117366.
PR 14-OCT-1993; US-136783.

PA (SMK) SMITHKLINE BEECHAM CORP.
PI (SMK) SMITHKLINE BEECHAM PLC.
PI Gross MS, Holmes SD, Sylvestre DR;
DR WPI; 95-123387/16.
DR P-PSDB; R70189.
PT Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT from high affinity mabs - useful in treatment of IL-4-mediated
PT and IgE-mediated allergic conditions
PS Disclosure; Fig.1; 9pp; English.
CC Spleen cells from mice immunized with human IL-4 were used to prepare
CC hybridomas, which were screened for anti-IL-4 MAb secretion. Only
CC clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC chains were cloned into pGEM7i+ and transformed into E. coli
CC DH5-alpha. The clones were sequenced (Q83490-91), and used for
CC antibody engineering.
SQ Sequence 396 BP; 99 A; 103 C; 103 G; 91 T;

Query Match 77.1%; Score 303; DB 14; Length 396;
Best Local Similarity 88.3%; Pred. No. 1.81e-181;
Matches 348; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 1 atggagacagacacatcctgtctatgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 60
|||||
Qy 1 ATGGAGTTCAGACACACTCTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGT 60
|||||
Db 61 gacattgtgtgacccaatctccaggtcttttgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
|||||
Qy 61 GACATTGCTGTCACACAGTCTCTGCTCTCTTAGGTGTATCTCTGGGGCAGAGGCCAC 120
|||||
Db 121 atctcctcgaaggccagccaaagtgttgattatgatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
|||||
Qy 121 ATCTCATGCGGGGGCCAGCAAAAGTGTCAGTACATCTGGCTATAGTTATATGCACTAGTAC 180
|||||
Db 181 caacagaacacaggaagacagccacccaaactcctcatctatgtgtgtgtgtgtgtgtgtgtgtgt 240
|||||
Qy 181 CAACAGAAACACGAGCAGACAGCCCAAACTCTCTATCTATCTTGCATCCACCTAGATCT 240
|||||
Db 241 gggatcccgacagcaggtttagtggaagtgggtgtgggtgtgggtgtgggtgtgggtgtgggtgt 300
|||||
Qy 241 GGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT 300
|||||
Db 301 cctgtggaggaggaggtgctgcaacctattactgtcagcaagtaagtgtgtgtgtgtgtgtgtgt 360
|||||
Qy 301 CCTGTGAGGAGGAGGATGCTGCAACCTATTACTGTGAGCAGACTAGGAGGATCCGTAC 360
|||||
Db 361 acgttgcgtggagccacaaagtgtgaaatcaaa 393
|||||
Qy 361 ACGTTCGAGGGGGACCAAGCTGGAATAAAAA 393
|||||

RESULT 5
ID Q92501 standard; cDNA; 399 BP.
AC Q92501;
DT 07-FEB-1996 (first entry)
DE Mouse antibody FB3-2 light chain variable region coding sequence.
KW Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
KW antibody; immunotolerance; animal; variegated display library;
KW variable region; antigen; immunorecessive; cell surface marker; foetal;
KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
KW familial hypercholesterolaemia; binding affinity; ds.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 67..399
FT /*tag= a

Jul 8 08:23

US-08-137-117B-24.mrg

9

```
QY 241 GGGGTCCTCCAGGTTGAGTCGAGTGGGTCTGGGACAGACTTCACCTCCACATCCAT 300
Db 307 cctgtgagagagagatactgcaacataattactgtcagcacagttggagatccgtac 366
QY 301 CTGTGGAGGAGGAGTGTCTGCAACTATTCTGTGACACAGTAGGGAATCCGTAC 360
Db 367 acgttcagaggggggacaaagctggaataaaa 399
QY 361 ACCTTCGGAGGGGACCAAGCTGGAAATAAAA 393
```

RESULT 7

```
ID Q98534 standard; DNA; 336 BP.
AC Q98534;
DT 27-FEB-1996 (first entry)
DE V1 coding sequence from an antibody against cancer-specific mucin.
KW Antibody; heavy chain; light chain; variable region; cancer; mucin;
KW hybridoma cell; murine; mouse; pancreatic cancer cell; expression vector;
KW Fv; human; constant domain; chimera; anaphylaxis; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 70..114
FT /tag= a
FT /note= "encodes CDR1"
FT misc_feature 160..180
FT /tag= b
FT /note= "encodes CDR2"
FT misc_difference 190..192
FT /tag= c
FT /transl_except= seq; GAG a.a.: Asp
FT misc_feature 277..303
FT /tag= d
FT /note= "encodes CDR3"
PN FR2714915-A1.
PD 13-JUL-1995.
PF 13-JAN-1995; 000349.
PR 13-JAN-1994; JP-002131.
PA (TOYO ) TOSOH CORP.
PI Chung Y, Iba Y, Kaneko T, Sowa M, Yasukawa K;
DR WP1; 95-247908/33.
DR P-PSDB; R80272.
PT New variable domains of antibody recognising cancer specific mucin
PT - and related DNA and expression vectors, producing chimeric
PT mouse-human antibody for diagnosis and treatment of cancer
PS Claim 8; Page 16-17; 25pp; French.
CC The nucleotide sequence of the variable region from the light chain of an
CC antibody against cancer-specific mucin. The coding sequence was isolated
CC from N2 hybridoma cells expressing a murine antibody reactive with
CC pancreatic cancer cells. The DNA encoding the antibody variable regions
CC from the heavy (Q98533) and light chains were isolated and inserted into
CC vectors. These vectors express the domains as an Fv antibody. Vectors
CC which additionally contain genes encoding the human constant domains
CC express a chimeric mouse-human antibody. The antibodies are useful in
CC the detection and treatment of cancer. The chimeras should be less likely
CC to cause anaphylaxis than the original murine antibody.
SQ Sequence 336 BP; 83 A; 92 C; 84 G; 77 T;
```

```
Query Match 75.6%; Score 297; DB 16; Length 336;
Best Local Similarity 94.6%; Pred. No. 2.03e-177;
Matches 315; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
```

```
Db 1 gacattgtctgacagctctctcttcttagctgtatctgtggcgagagggccacc 60
|||||
```

Jul 8 08:23

US-08-137-117B-24.mrg

10

```
QY 61 GACATTGCTGCACACAGTCTCTGCTTCTTAGGTGTATCTCTGGGCGAGAGGCCACC 120
Db 61 atctcatgcaggcgccagcaaaagtgtcactacatctgacttttagttatgtcaactgggtac 120
QY 121 ATCTCATGCGAGGGCCAGCAAAAGTGTGATCATCTGGCTATAGTTATATGCACTGGTAC 180
Db 121 caacagaacccgggagacgaccccaaacctctctctatctgtgacctcaaacctagaatct 180
QY 181 CAACAGAAACACAGGACAGACACCCAAACTCCTCATCTATCTTGCATCCAACTAGAAATCT 240
Db 181 ggggtccctgagaggttcagtgcgagtcgggtctgggacagagacttcacctcaacatccat 240
QY 241 GGGGTCCCTCCAGGTTTCAGTGGCATGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300
Db 241 cctgtggagagagagtgctgcaacctattactgtcagcacagtagggagttccgtg 300
QY 301 CTGTGGAGGAGGAGTGTCTGCAACTATTACTGTGACACAGTAGGGAATCCGTAC 360
Db 301 acgttcgtgtgagggacccaaactggaataaaa 333
QY 361 ACCTTCGGAGGGGACCAAGCTGGAAATAAAA 393
```

RESULT 8

```
ID Q36609 standard; DNA; 393 BP.
AC Q36609;
DT 02-JUN-1993 (first entry)
DE Anti-CD4 antibody MT 3.10 light chain variable region.
KW immunosuppression; tissue transplantation; graft; L chain; V region;
KW T-helper cell inhibition; transplant rejection; Mab;
KW interleukin-2 receptor; ss.
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT /tag= a
FT mat_peptide 61..393
FT /tag= b
FT /note= "V1 region begins at position 361"
PN DE4143214-A.
PD 28-JAN-1993.
PF 30-DEC-1991; 143214.
PR 25-JUL-1991; DE-124759.
PR 30-DEC-1991; DE-143214.
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
PI Kaluza B, Rietmueller G, Scheuer W, Weidle U;
DR WP1; 93-037582/05.
DR P-PSDB; R32123.
PT Synergistic antibody compsn. for use as immunosuppressant -
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
PT alpha- or anti-IL2R beta antibodies
PS Claim 5; Page 11; 18pp; German.
CC This sequence encodes the light chain variable region of a preferred
CC anti-CD4 monoclonal antibody for use in the claimed synergistic
CC composition. Mab MT 3.10 is deposited as clone 3.101/sB10 (ECACC
CC 90090702). The anti-CD4 antibody is used with at least one anti-IL2R
CC alpha or beta antibody. Individually the antibodies are strongly
CC inhibiting and when used together their immunosuppressive properties
CC are improved; they synergistically inhibit T-helper cell
CC proliferation to effectively inhibit transplant rejection at low
CC doses without significantly reducing the general immune response.
CC See Q36607-Q36616.
SQ Sequence 393 BP; 100 A; 105 C; 98 G; 90 T;
```

```
Query Match 75.1%; Score 295; DB 6; Length 393;
Best Local Similarity 87.5%; Pred. No. 4.53e-176;
```

Matches	344;	Conservative	0;	Mismatches	49;	Indels	0;	Gaps	0;
Db	1	atggagagacacacaatcctgctatgggtgctgctgctgctgggtccaggctccaatggt	60						
Qy	1	ATGGAGTCAGACACACTTCGTGTGGGTACTGCTGCTGGGTTCGAGGTTCCACTGGT	60						
Db	61	gacattgtgtgacccaattccagctcttttgccctatgtctctaggcagagggccacc	120						
Qy	61	GACATTGCTGACACAGTCTCTCTGCTTCTTAGGTATCTCTGGGCAGAGGGCCACC	120						
Db	121	atctcctgcaaggccagccaagtcttgattatgatggtgatgtatatgaactgggtac	180						
Qy	121	ATCTCATGCGAGGGCCAGCAAAAGTGCAGTACATCTGGCTAGTATATGTCACCTGGTAC	180						
Db	181	caacgaaacaggagacagccaccacaaactcctctatgtctgcatcaatctagaatct	240						
Qy	181	CAACGAAACAGGACAGACACCCAACTCCTCATCTATCTTGGCATCCAACTTGATCT	240						
Db	241	gggattcccgccagattt agtggcagtggggtccggagacagcttcacccctcaactccat	300						
Qy	241	GGGGTCCCTCCGACGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCAT	300						
Db	301	cctgtggagagaggagatgctgcacacctattactgtcacgaagt agtgaggtacctcg	360						
Qy	301	CCTGTGGAGGAGGAGGATGCTGCACACCTATTACTGTGCACAGCTAGGAGGAATCCGTAC	360						
Db	361	acgttcgtgtggaggcaccacagctggaaatacaaa	393						
Qy	361	ACGTTCTGGAGGGGGACCAAGTGTGAAATAAAA	393						

RESULT	9	
ID	Q30757 standard; cDNA; 393 BP.	
AC	Q30757;	
DT	30-MAR-1993 (first entry)	
DE	p64-k4.	
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;	
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;	
KW	plasmid; p64-k4; p64-h2; ss.	
OS	Synthetic.	
EH	Key	Location/Qualifiers
FT	sig_peptide	1..60
FT	/*tag= a	
FT	mat_peptide	61..393
FT	/*tag= b	
PN	W09219759-A.	
PD	12-NOV-1992.	
PF	24-APR-1992; J00544.	
PR	25-APR-1991; JP-095476.	
PR	19-FEB-1992; JP-032084.	
PA	(CHUS) CHUGAI SEIYAKU KK.	
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;	
DR	WPI; 92-398882/48.	
DR	P-PSDB; R29008.	
PT	Reconstituted human antibody to human interleukin-6 receptor -	
PT	has low antigenicity and contains mouse V-region complementarity	
PT	determining regions	
PS	Disclosure; Page 124-125; 207pp; Japanese.	
CC	The sequences given in Q30757-58 were used in example to illustrate	
CC	the production of a human antibody which recognises human	
CC	interleukin-6 receptor (IL-6R). The antibody comprises light (L)	
CC	chain and heavy (H) chain variable regions which were derived from a	
CC	mouse monoclonal antibody produced from the hybridoma AUK64-7 which	
CC	contained the plasmids p64-k4 and p64-h2.	

SQ Sequence 393 BP; 93 A; 101 C; 100 G; 99 T;
 Query Match 74.6%; Score 293; DB 5; Length 393;
 Best Local Similarity 87.3%; Pred. No. 1.01e-174;
 Matches 343; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 Db 1 atggatgcagacacactcctgctatgggtgctgctctctgggttcagggtccacaggt 60
 Qy 1 ATGGAGTCAGACACACTCCTGCTATGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGCT 60
 Db 61 gacattgtgttgatccaactctccaggtcttcttgggtgtgtctctaggcgagaggccacc 120
 Qy 61 GACATTGTGCTGCAGACAGTCTCTGCTCTCTTAGGTGTATCTCTGGGGCAGAGGGCCACC 120
 Db 121 atactctgcagagccagtgaaagtgttgatgtatggcaatagttttagtgcactgggtac 180
 Qy 121 ATCTCATGAGGGCGGAGAAAGTGTCACTACATCTGGCTAGTATTATATGCACTGGTAC 180
 Db 181 cagcagaacacagcagcagccaccacaaactctcatctatcgtgcataccactagaatct 240
 Qy 181 CAACAGAAACAGACAGACAGACCCCAAACTCCTCATCTATCTTGCAATCCAACCTAGAACT 240
 Db 241 gggatccctgccaggttcagtgccagtggtctaggacagacttcacccctcaccattaat 300
 Qy 241 GGGTCCCTGCCAGGTTCACTGGCAGTGGGCTCGGACAGACTTCACCTCAACATCCAT 300
 Db 301 cctgtggaggtgatgatgtgtgcaacctattactgtcagcaagaatgaggatccccc 360
 Qy 301 CCTGTGGAGGAGGAGATGCTGCAACTTACTTACTCAGCACAGTAGGAGAATCGGTAC 360
 Db 361 acgttcggtgctggaccagctggagctgaaa 393
 Qy 361 ACGTTCGGAGGGGGGACCAAGCTGGAAATAAA 393
 RESULT 10
 ID Q90421 standard; DNA; 330 BP.
 AC Q90421;
 DT 19-JAN-1996 (first entry)
 DE DNA encoding immunoglobulin light chain of anti-idiotype antibody
 DE against human anticancer antibody.
 KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
 KW complementarity determining region; ss.
 OS Mus sp.
 PN J07101999-A.
 PD 18-APR-1995.
 PF 06-OCT-1993; 272950.
 PR 06-OCT-1993; JP-272950.
 PA (HAGI/) HAGIWARA Y.
 DR WPI; 95-182987/24.
 DR P-PSDB; R74956.
 PT Novel anti-idiotype antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.
 PS Claim 19; Page 5; 28pp; Japanese.
 CC Q90420-Q90424 are DNA molecules encoding possible light chains of a new
 CC anti-idiotype antibody against a human anticancer monoclonal antibody. This
 CC antibody contains in its heavy chain 3 complementarity determining region
 CC CDR1 (R74929-R74931), CDR2 (R74932-R74935) and CDR3 (R74936-R74939),
 CC this is also true of the light chain which has its own CDR1
 CC (R74944-R74946 and R85774), CDR2 (R74947-R74949) and CDR3 (R74950-R74954
 CC The antibody and DNA encoding it are useful in pharmacological, medical
 CC and biochemical fields.
 SO Sequence 330 BP; 85 A; 86 C; 85 G; 74 T;

Query Match 73.8%; Score 290; DB 16; Length 330;
Best Local Similarity 95.8%; Pred. No. 1.07e-172;
Matches 319; Conservative 0; Mismatches 11; Indels 3; Gaps 2;

```
Db 1 gacattgtgtgacacagtcctctcttcttagctgtatctctgtggcagagggcctcc 60
    |||||||
Qy 61 GACATTGCTGCACACAGTCTCTCTTCTTAGGTGTATCTCTGGGCGAGAGGCCACC 120
    |||||||
Db 61 atctcatacaggccagcaaaagtgtgagtcacatctggctatagttatgtacgtggaac 120
    |||||||
Qy 121 ATCTATGTCAGGCGCAGCAAAAGTGTGAGTACATCTGGCTATATAGTTATATGCACTGGTAC 180
    |||||||
Db 121 caacagaaacaggacagccacagcactcctcatctgtatctgtatccaacctagaatct 180
    |||||||
Qy 181 CAACAGAAACAGGACAGACACCAAACTCCTCATCTATCTTGCATCCAACTAGAAATCT 240
    |||||||
Db 181 ggggtccctccaggttcagtgagcagtggtgtggacagagcttcacccccaacatccat 240
    |||||||
Qy 241 GGGGTCCCTCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300
    |||||||
Db 241 cctgtgagggagggatgtgcacactattactgtcagcacattagggtgag--cttac 297
    |||||||
Qy 301 CTTGTGGAGGAGGAGTGTGCAACCTATTACTGTGACGACAGTAGGGAGAAATCCGTAC 360
    |||||||
Db 298 acgttcggaggggggaccaaagctggaataaaa 330
    |||||||
Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAATAAAA 393
    |||||||
```

RESULT 11

```
ID Q90422 standard; DNR; 330 BP.
AC Q90422;
DT 22-JAN-1996 (first entry)
DE DNA encoding immunoglobulin light chain of anti-idiotypic antibody.
DE against human anticancer antibody.
KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW complementarity determining region; se.
OS Mus sp.
PN J07101999-A.
PD 18-APR-1995.
PF 06-OCT-1993; 272950.
PR 06-OCT-1993; JP-272950.
PA (HAG1/) HAGIWARA Y.
DR WPI; 95-182987/24.
DR P-PSDB; R74958.
PT Novel anti-idiotypic antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
PS Claim 20; Page 5; 28pp; Japanese.
CC Q90420-Q90424 are DNA molecules encoding possible light chains of a new
CC anti-idiotypic antibody against a human anticancer monoclonal antibody. This
CC antibody contains in its heavy chain 3 complementarity determining regions
CC CDR1 (R74929-R74931), CDR2 (R74932-R74935) and CDR3 (R74936-R74939),
CC this is also true of the light chain which has its own CDR1
CC (R74944-R74946 and R85774), CDR2 (R74947-R74949) and CDR3 (R74950-R74954)
CC The antibody and DNA encoding it are useful in pharmacological, medical
CC and biochemical fields.
SQ Sequence 330 BP; 84 A; 88 C; 85 G; 73 T;
```

Query Match 72.8%; Score 286; DB 16; Length 330;
Best Local Similarity 95.2%; Pred. No. 5.31e-170;
Matches 317; Conservative 0; Mismatches 13; Indels 3; Gaps 2;

```
Db 1 gacattgtgtgacacagtcctctcttcttagctgtatctctgtggcagagggcacc 60
    |||||||
Qy 61 GACATTGCTGCACACAGTCTCTCTTCTTAGGTGTATCTCTGGGCGAGAGGCCACC 120
    |||||||
Db 61 atctcatacaggccagcaaaagtgtgagtcacatctggctatagttatgtacgtggaac 120
    |||||||
Qy 121 ATCTATGTCAGGCGCAGCAAAAGTGTGAGTACATCTGGCTATATAGTTATATGCACTGGTAC 180
    |||||||
Db 121 caacagagacaggacagccacagcactcctcatctatctgtatccaacctagactct 180
    |||||||
Qy 181 CAACAGAAACAGGACAGACACCAAACTCCTCATCTATCTTGCATCCAACTAGAAATCT 240
    |||||||
Db 181 ggggtccctccaggttcagtgagcagtggtgtggacagagcttcacccccaacatccat 240
    |||||||
Qy 241 GGGGTCCCTCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300
    |||||||
Db 241 cctgtgagggagggatgtgcacactattactgtcagcacattagggtgag--cttac 297
    |||||||
Qy 301 CTTGTGGAGGAGGAGTGTGCAACCTATTACTGTGACGACAGTAGGGAGAAATCCGTAC 360
    |||||||
Db 298 acgttcggaggggggaccaaagctggaataaaa 330
    |||||||
Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAATAAAA 393
    |||||||
```

RESULT 12

```
ID Q71394 standard; cDNA; 331 BP.
AC Q71394;
DT 25-APR-1995 (first entry)
DE Anti-carcinoembryonic antigen chimeric light chain Ab, cDNA.
KW Anti-carcinoembryonic antigen chimeric antibodies; CEAS;
KW chimeric human-murine; breast or colorectal carcinoma;
KW light chain; ds.
OS Chimeric Mus muscaris.
OS Chimeric Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..331
FT /*tag= a
PN W09419466-A.
PD 01-SEP-1994.
PF 16-FEB-1994; U01709.
PR 16-FEB-1993; US-017570.
PA (DMC ) DOW CHEM CO.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Gourlie BB, Kaplan DA, Mezes PS, Rixon MW, Schlom J;
DR WPI; 94-294331/36.
DR P-PSDB; R60564.
PT Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis
PT and therapy of carcinoma, e.g. breast or colorectal carcinoma
PS Claim 1; Page 49; 67pp; English.
CC Q71394 codes for R60564 the antibody light chain region of
CC murine-human anti-carcinoembryonic antigen (CEA) chimeric
CC antibody. Which can be used in in vitro immunoassays for
CC the detection of CEA, and monitoring of tumour-associated
CC antigen during therapy. It can also be used in vivo diagnostically,
CC or in therapy for the treatment of tumours associated with
CC colorectal and breast carcinomas, as well those of the
CC gastrointestinal tract, lung, ovary and pancreas.
SQ Sequence 331 BP; 81 A; 93 C; 83 G; 74 T;
```

Query Match 72.8%; Score 286; DB 12; Length 331;
Best Local Similarity 95.2%; Pred. No. 5.31e-170;
Matches 317; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

Db	1	gacattgtgtgacacagctctcctgttctcttaactgtatctctgggtgagggccaacc	60
Qy	61	GACATTGTGCTGACACAGCTCTCCTGCTTCTTTAGTGTATCTTGGGCGAGAGGCCACC	120
Db	61	atctcatgcaggggccagcaaaagtgcadtgcattcgtgttatagttatatgcactgggtac	120
Qy	121	ATCTCATCGAGGGCGACGAAAGTGCAGTACATCTGGCTATAGTTATATGCACCTGGTAC	180
Db	121	caacagagaccaggagacgcaccaccaactcctcatctatcttgcattccaacctacaatct	180
Qy	181	CACAGAAACCGACGACAGACACCCAACTCCTCATCTATCTTGCAATCCAACTTGAATCT	240
Db	181	ggggtccctgccagggttcadtggcagtggggtcgggacagacttcacctcaacatccat	240
Qy	241	GGGGTCCCTCGCAGGTTGAGTGGCAGTGGGCTTGGGACACACTTCACTCCCTCAACATCAT	300
Db	241	cctgtggaggaggaggtatgtgcaacctattactgtcagcacagtaggggattccg---	297
Qy	301	CCGTGGAGGAGGAGAGTCTGCAACTTATTACTGTGAGCAGTAGGGAGAAATCCGTAC	360
Db	298	acgttcggtggaggccaccaagctggaatcaaa	330
Qy	361	ACCTTCGAGGGGGGACCAAGCTTGAAATAAA	393

RESULT	13	
ID	Q34575 standard; DNA; 393 BP.	
AC	Q34575;	
DT	10-MAY-1993 (first entry)	
DE	Antibody 4A2 light chain constant region, p4A2K-13.	
KW	Fd' ; fragment; human; 4A2; constant region; Fab' ; F(ab')2; antibody;;	
OS	light chain; primer; ss.	
PN	Mus musculus.	
PD	W09222324-A.	
PR	23-DEC-1992.	
PF	15-JUN-1992; U04976.	
PP	14-JUN-1991; US-714175.	
PA	(XOMA) XOMA CORP.	
PI	Better MD, Carroll S, Horwitz AH;	
PT	WPI: 93-017909/02.	
DR	N-PSDB; R30881.	
PT	Polynucleotide sequences encoding Fab' and F(ab')2 fragments -	
PT	used to produce, e.g. antibody-ricin A chain immuno:toxin(s)	
PS	Disclosure; Fig 10; 92pp; English.	
CC	This sequence encodes the light chain constant (CL) from	
CC	mouse antibody 4A2. This sequence was used in conjunction	
CC	with the Fd' sequences given in Q34567-72 to produce chimeric Fd'	
CC	vectors.	
CC	Sequence 393 BP; 93 A; 97 C; 108 G; 95 T;	

Query Match 72.5%; Score 285; DB 6; Length 393;
Best Local Similarity 86.3%; Pred. No. 2.51e-169;
Matches 339; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

[illegible]

Qy	121	ATCTCATGCGGGCGAGAAAGTGTGCTAGTACATCTGGCTATAGTTATATGCACTGGTAC	180
Db	181	caacagaacaacaggacagccaccaccaactcctcatctatgctgcataccaacgtagaatct	240
Qy	181	CACAGAACCAAGGACAGACACCAACCTCTCATCTATCTTGCATCCAACTCAGAACTC	240
Db	241	ggggtccctccaggtttagtggcagtgggtcgtggaacagacttcagcctcaaatccat	300
Qy	241	GGGGTCCCTGCCAGGTTGAGTGGCACTGGGTCTGGGACAGACTTCACCTCAACATCCAT	300
Db	301	ccctgtggggagagagatattggagatgtattctgtccaagagagtaggaaaggttccttgg	360
Qy	301	CCTGTGGAGGAGGAGTGTGCAACCTATTACTGTGACACAGTAGGGAGAAATCCGTAC	360
Db	361	acgttcggtggagggaccacagctggaatcaaa	393
Qy	361	ACGTTGCGAGGGGGACCAAGCTGGAAAAATAAA	393

RESULT	14
ID	Q12683 standard; DNA; 335 bp.
AC	Q12683;
DT	01-OCT-1991 (first entry)
DE	Murine IB4 light chain-1 variable region.
DE	Monoclonal antibody; complementary determining region; CDR;
KW	interferon; hybriidoma 194; protein R2I; Gal/Rel; Ig; ss.

DE Antibody 4A2 light chain constant region, p4A2K-13.
KW Fd'; fragment; human; 4A2; constant region; Fab'; F(ab')₂; antibody;
KW light chain; primer; ss.

Query Match 72.5%; Score 285; DB 6; Length 393;
Best Local Similarity 86.3%; Pred. No. 2.51e-169;
Matches 339; Conservative 0; Mismatches 54; Indels

Db 1 atggagtgcagacacactcctgctatgggtgctgctctctgggtccaggctccactggt 60
|||||
Qy 1 ATGGAGTGCAGACACACTCCTGCTATGGGTACTGCTCTGCGTCTGGGTCCAGGTCGACTGGT 60

Db	121	caacagaacccaggacagccaccagactcctcatctatcttgtatccaacctaagaatct	180
Qy	181	CAACAGAAAACGAGCAGACAGACCACCAACTCCTCATCTATCTTGGCATCCAACCTAGAACTCT	240
Db	181	gggggtccctgccaggttcagtgggcagtggtctaggacagactcaccctcaacatccat	240
Qy	241	GGGGTCCCTGCCAGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATCCAT	300
Db	241	cctgtggaggaggagatgctgcaaccttactgttcagcaattaggagc-t----tac	296
Qy	301	CCCTGTGGAGGAGGAGGATGCTGCCAACTTACTTCTCAGCACAGTAGGGGAGAATCCGTAC	360
Db	297	acgttcggaggggggacacagctggaataaaa	329
Qy	361	ACGTTTCGGAGGGGGGACCAAGCTGGAATAAAA	393

RESULT	15	
ID	Q74148 standard; DNA; 336 BP.	
AC	Q74148;	
DT	01-FEB-1996 (first entry)	
DE	Human thyroid stimulating hormon antibody light chain variable region.	
DE	Human thyroid stimulating hormone; TSH; human; variable region; light;	
KW	thyroid stimulating hormone; TSH; human; variable region; light;	
KW	chain; antibody; chimeric antibody; ss.	
OS	Homo sapiens.	
PN	J07132097-A.	
PD	23-MAY-1995.	
PF	28-JUN-1993; 156707.	
PR	28-JUN-1993; JP-156707.	
PA	(TOYJ) TOSOH CORP.	
DR	WPI; 95-220118/29.	
PT	DNA encoding an antibody recognising human thyroid-stimulating	
PT	hormone - and preparation of chimeric antibody by expressing the	
PT	DNA in a transformed host cell	
PT	Claim 8; Fig 4; 8pp; Japanese.	
CC	The DNA encodes the light chain variable region of an antibody	
CC	recognising human thyroid stimulating hormone (hTSH). Prepn. of a	
CC	chimeric antibody by expressing the DNA in a transformed host cell	
CC	is also claimed. The anti-hTSH antibody has an additional useful	
CC	function which could not be given by a mouse derived anti-TSH monoclonal	
CC	antibody (sic).	
SQ	Sequence 336 BP; 85 A; 94 C; 81 G; 76 T;	

Query Match 72.0%; Score 283; DB 16; Length 336;
Best Local Similarity 92.5%; Pred. No. 5,59e-168;
Matches 308; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Db	1	gacattgctgacacagtcctctcgtctctcttaoctgtatctctcgtggacagagggccacc	60
Qy	61	GACATTTGTGCTGACACAGTCCTCCTGCTTCCTTAGGTGTATCTCTGGGCGACAGGGCGACC	120
Db	61	atctcatgcaggccagccagagtcacgttccatctagctatagttatatgcactgggtac	120
Qy	121	ATCTCATTCGACGGCGCAGAAAGTGTCTAGTACATCTGGCTATAGTTATATGCACTGGGTAC	180
Db	121	caacagaacacaggacagccaccacaaactcctcatcaagtttgcataccaaactagaatct	180
Qy	181	CAACAGAAACAGACAGACACCCCAACTCCCTCATCTACTTTGCATCCAACTTAGANTCT	240
Db	181	gggggtccctgccagggttcagtcggcagtggggtctggagacagacttcaacctccaatccat	240
Qy	241	GGGGTCCCTGCCAGGTTTCAGTGGAGTGGGTCTGGACAGACTTCACCCCTCAACATCCAT	300

Db 241 cctgtggaggagacagtgtgcaacatactactgcaacacacttggagagattcctcgg 300
 Qy 301 CCTGTGGAGGAGGAGTCTGCAACCTATTACTGTGACACAGTAGGGGAATCCGTAC 360
 Db 301 acgttcggtggaggcaccacgttgaaatacaa 333
 Qy 361 ACGTTTCGAGGGGGGACCAACTCGAAATAAAA 393

Search completed: Mon Jul 8 08:34:22 1996
Job time : 47 secs.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Db 121 atctatcacagggccagcaaaaagtgcagtaacctgtggtatagttatgtatgcaciggaac 180
|||||
Qy 121 ATCTCATGCGAGGGCCAGCAAAAAGTGTGAGTACATCTGGCTATAGTTATATGCACTGGTAC 180

Db 181 caacagaaccaggagcagccaccagactcctcatctatctgtatccaacctagaatct 240
|||||
Qy 181 CAACAGAAACCGAGACAGACCAAACTCTCATCTATCTTGCATCCACCTAGAACTCT 240

Db 241 ggggtccctgccaggttcagtgcaagtgggtctggacagattccacctcaacatccat 300
|||||
Qy 241 GGGGTCCCTGCCAGGTTCAGTGCGAGTGGGTCTGGGACAGACTTACCCTCAACATCCAT 300

Db 301 cctgtgagagagagatgcctcaacctattactcagcacatlaggagg-tc--tac 357
|||||
Qy 301 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTACGACAGTAGGGAGAAATCCGTAC 360

Db 358 acgttcgaggggggaccagagctggaataaaa 390
|||||
Qy 361 ACGTTGGAGGGGGACCAAGCTGGAAATAAAA 393

RESULT 3
LOCUS MMIGKV386 390 bp RNA ROD 24-OCT-1995
DEFINITION M.musculus mRNA for Ig kappa light chain variable region (cell line 386).
ACCESSION X91670
KEYWORDS complementarity determining region;
immunoglobulin variable region; kappa light chain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha;
Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 390)
AUTHORS Carceller,A., Rosell-Vives,E., Gomez-Roig,A., Adan,J., Sproll,M.
and Puilat,J.
TITLE Immunological and structural properties of anti-idiotypic antibodies mimicking an epitope of human epidermal growth factor receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 390)
AUTHORS Rosell-Vives,E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-1995) to the EMBL/GenBank/DDBJ databases. E.
Rosell-Vives, MERCK, Farma y Quimica S.A., Caspe 108, E-08010 Barcelona, SPAIN
COMMENT NCBI gi: 1001882
FEATURES
source
location/Qualifiers
1..390
/organism="Mus musculus"
/strain="BALB/c"
/sub_strain="by J Ico"
/tissue_type="hybridoma"
/cell_type="fusion of splenocytes x HL1 friendly myeloma 653"
/cell_line="386"
/chromosome="6"
1..60
sig_peptide
CDS 1..>390
/note="pid:e200732; NCBI gi: 1008127"
/codon_start=1
/product="immunoglobulin kappa light chain"
/translation="NESDTLLWLLWPGTGDIVLTQSPASLAVSLQRATISYR

AKSVSTSCYSYHNNQKPCQPRLIIYVSNLESCVPARESCSGDFTTINIHPV
EEDASTYYCOHIREVYTFGGGKLEIK"
1..390
V_region
/product="variable region of Ig kappa light chain"
misc_feature 130..174
/note="complementarity-determining region 1"
/product="CDR1"
misc_feature 225..240
/note="complementarity-determining region 2"
/product="CDR2"
misc_feature 340..360
/note="complementarity-determining region 3"
/product="CDR3"
BASE COUNT 96 a 103 c 100 g 91 t
ORIGIN

Query Match 89.1%; Score 350; DB 82; Length 390;
Best Local Similarity 96.4%; Pred. No. 0.00e+00;
Matches 379; Conservative 0; Mismatches 11; Indels 3; Gaps 2;

Db 1 atggagtcagacacactcctgctatgggtactgctgtctgtgggtccagggtccactggt 60
|||||
Qy 1 ATGGAGTGCAGACACACTCCTGCTATGGGTACTGCTGCTGTGGGTTCCAGGTTCCACTGGT 60

Db 61 gacattgtgtgacacagtctctgttccttagctgtatctctgtgggagagggccacc 120
|||||
Qy 61 GACATTGTGCTGACACAGTCTCTGCTCTCTTAGTGTATCTCTGGGCGAGGGGCCACC 120

Db 121 atctcatcagggccagcaaaagtgcagtcacatctggctatagttatgtatgcactggaac 180
|||||
Qy 121 ATCTCATGCGAGGGCCAGCAAAAAGTGTGATCTGCTATAGTTATATGCACTGGTAC 180

Db 181 caacagaaccaggagcagccaccagactcctcatctatctgtatccaacctagaatct 240
|||||
Qy 181 CAACAGAAACCGAGACAGACACCAAACTCCTCATCTATCTTGCATCCACCTAGAACTCT 240

Db 241 ggggtccctgccaggttcagtgcaagtgggtctggacagattccacctcaacatccat 300
|||||
Qy 241 GGGGTCCCTGCCAGGTTCAGTGCGAGTGGGTCTGGGACAGACTTACCCTCAACATCCAT 300

Db 301 cctgtgagagagagatgcctcaacctattactcagcacatlaggagg-tc--tac 357
|||||
Qy 301 CCTGTGGAGGAGGATGCTGCAACCTATTACTGTACGACAGTAGGGAGAAATCCGTAC 360

Db 358 acgttcgaggggggaccagagctggaataaaa 390
|||||
Qy 361 ACGTTGGAGGGGGACCAAGCTGGAAATAAAA 393

RESULT 4
LOCUS MMIGVKP 429 bp RNA ROD 04-AUG-1992
DEFINITION Mouse mRNA for nonfunctionally rearranged Ig-kappa V/Jk2 region.
ACCESSION X05184 M31709
KEYWORDS Ig kappa light chain; Ig light chain.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 429)
AUTHORS Strohal,R., Kroemer,G., Wick,G. and Kofler,R.
TITLE Complete variable region sequence of a nonfunctionally rearranged

JOURNAL MEDLINE	kappa light chain transcribed in the nonsecretor P3-X63-Ag8.653 myeloma cell line 871174798
COMMENT	The nonfunctional transcript shows 98% homology to the Balb/c Vk21-E germline gene. Data kindly reviewed (18-May-1988) by Strohal R.

```

NCBI gi: 52542
FEATURES
source
    1..429
        /organism="Mus musculus"
        /strain="Balb/C"
        /cell_line="myeloma P3-X63-Ag8.653"
    prim_transcript
        1..>429
        /notes="primary transcript"
    misc_feature
        41..100
        /notes="leader peptide (AA -20 to -1
    misc_feature
        101..393
        /notes="Vk segment"
    misc_feature
        393..394

```

BASE COUNT	108 a	116 c	107 q	98 t
BASE COUNT	108 a	116 c	107 q	98 t

Query Match 87.8%; Score 345; DB 54; Length 429;

Best Local Similarity 96.4%; Pred. No. 0.00e+00;
Matches 379; Conservative 0; Mismatches 10; Indels 4; Gaps 2;

D_b 41 atggagacagacacactcctgttatgggtactgctgctctgggtccagggtccactggt 100

Qy 1 ATGGAGTCAGACACACTCTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGT 60

Db 101 gacattgtgctgacacagtcctcctgcttccttcccttagctgtatctctgggcagagggccacc 160

Qy 61 GACATTGTGCTGACACAGTCTCCTGCTTCTTGGGACAGGGCCACC 120

Db 161 atctcatacagggccagcaaaagtgtcagtagcatctggctatagttatatgcactggaac 220

Qy 121 ATCTCATGAGGGCCAGCAAAAGTCTCAGTACATCTGGCTATAGTTATATGCACTGGTAC 180

D_b 221 caacagaaaccaggacagccaccagactcctcatctatcttqtatccaacctagaatct 280

181 CAACAGAAACCGGACAGACACCCAAACTCCTCATCTATCTTTGCATCCAACTAGAATCT 240

Db 281 qgggtccctgccaggttcagtggcagttgggtctcggacagacttcacccctcaacatccat 340

QY 241 GGGGTCCTGCCAGGTTCACTGGCACTGGGTCTGGGACAGACTTACCCCTACATCCAT 300

Db 341 cctctgagaggaaggaatcttcaacctattactctcagcacattagggagc-t---tac 396

QV 301 CCTGTGGAGGAGGAGTCTGCACCTATTACTCTCAGCACAGTAGGGAGAAATCCGATC 360

Db 397 acgttcgagagggagaccgaagctgaaataaaa 429

QV 361 ACGTTTCGGAGGGGGACCAAGCTGGAAATAAAA 393

RESULT 5

LOCUS	MUSTGKCSU	444 bp	mRNA	ROD	12-JUN-1993
DEFINITION	Mouse Ig aberrantly rearranged kappa-chain mRNA V-J2-C-region, complete cds.				

ACCESSION M35669
KEYWORDS C-region; J-region; V-region; immunoglobulin light chain;

SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
Immunoglobulin-kappa.					
Mouse myeloma MOPC-21, cDNA to mRNA.					
Mus musculus					
Eukaryota; Animalia;					
Eutheria; Chordata;					
Eutheria; Rodentia;					
Myomorpha; Muridae;					
Murinae.					
1 (bases 1 to 444)					
Carroll, W. L., Mendel, E. and Levy, S.					
Hybridoma fusion cell lines contain an aberrant kappa transcript					
Mol. Immunol. 25, 991-995 (1988)					

COMMENT	NCBI gi: 197295
FEATURES	Location/Qualifiers
source	1..444
	/organism="Mus musculus"
sig_peptide	28..87
	/note="Ig kappa-chain V-J2-C-region signal peptide"
	/codon_start=1
CDS	28..414
	/notes="Ig kappa-chain V-J2-C-region precursor; NCBI gi: 309369"

```

/codon_start=1
/translation="METDTLLWLLWPGSTGIVLTQSPASVLSIGQRTISYR
ASKVSTSGYSMHWQKQPGQPRLLIYVSNLSEGVPAFSGSGSDFTLNIHPV
EEEDAAITYCOHIRELTIRSGGSPSWK"

```

mat_peptide

```
mac_peptide
00:111
/note="Iq kappa-chain V-J2-C-region"
```

BASE COUNT	108 a	122 c	111 g	103 t
ORIGIN	Chromosome 6.			

Query Match 87.8%; Score 345; DB 56; Length 444;
Best Local Similarity 96.4%; Pred. No. 0.00e+00;
Matches 379; Conservative 0; Mismatches 10; Indels 4; Gaps 2;

Db 28 atggagacagacacactcctgttatgggtactgctgctggttccaggttccactggt 87

QY ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QV 1 ATGAGTCAGACACTCCTGCTATGGGTACTGCTGCTCTGGTTCAGGTTCCACTGGT 60

Db 88 gacattgtgtgacacagtctcctgcttccttagctgtatctctggggcagagggccacc 147

61 GACATTGCTGCACACAGTCTCCCTGCTTCCCTAGGTGTAATCTCTGGGGCAGAGGGCCACC 120

Db 148 atctcatacagggccagcaaaagtgtcagtcacatctggctatagttatatgcactggaac 207

QY 121 ATCTCATGAGGGCCAGCAAAAAGTGCAGTACATCTGGCTATAGTTATATGCACCTGGTAC 180

Db 208 caacagaaaccaggacagccaccagactcctcatctatcttqtatccaacctagaatct 267

QY 181 CAACAGAACCCAGGACAGACACCCAAACTCCTCATCTATCTTGATCCGACCTAGAATCT 240

Db 268 ggggtccctgcagatttcagtcggcagtcgggtctcggacagacttcacccctcaacatccat 327

Qy 241 GGGGTCCCTGCCAGGTTCA GTGGCAGTGGGTCTGGGACAGACTTCACCCCTCAACATTC CAT 300

Db 328 cctgtggaggaggagatgctgcaacctattactgtcagcacattaggagc-t---tac 383

301 CCCTGGAGGAGGAGATGCTGCAACCTATTACTGTGAGCAGATAGGGAGAAATCCGTAC 360
QY

Db 384 acgttcggagggggggaccaagctggaataaaa 416

QY 361 ACGTTCGAGGGGGACCAAGCTGGAATAAAA 393

RESULT 6

Jul 8 08:22

US-08-137-117B-24.fge

11

Qy 181 CAACAGAAACGAGGACAGACACCAAACTCCTCATCTATCTTCATCCACCTAGAACTCT 240
Db 181 ggggtccctnccaggttcagtnccagtggtctcggagacagacttcacccctcaacatccat 240
Qy 241 GGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300
Db 241 cctgtggagaggaggtcgtgcaacctattactgtcagcacagtagtagggaggttcctgac 300
Qy 301 CCTGTGGAGGAGGAGGATGCTGCACCTATTACTGTGACGACAGTAGGAGAATCCGTAC 360
Db 301 acgttcggagggggaccagagctggaataaaa 333
Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAATAAAA 393

RESULT 8
LOCUS MMT3VL 333 bp DNA ROD 05-DEC-1993
DEFINITION M. musculus anti-T3 980Q variable light chain.
ACCESSION X67467 S40893
KEYWORDS light chain; monoclonal antibody; variable region.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorphia; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 333)
AUTHORS Thammara, P., Gaito, A.L. and Largen, M.T.
TITLE Sequences of variable regions of a monoclonal antibody specific to the thyroid hormone, triiodo-L-thyronine
JOURNAL Mol. Immunol. 29 (7-8), 1025-1028 (1992)
MEDLINE 92342145

COMMENT NCBI gi: 395286
FEATURES
source
1..333
/organism="Mus musculus"
/sex="female"
/strain="CBA/J"
/cell_line="hybridoma 980Q"
/sub_clone="980Q 321.22.32.12"
<1..>333
/note="light chain"
/product="anti-T3 antibody 980Q"

BASE COUNT 83 a 91 c 83 g 76 t
ORIGIN
Query Match 78.1%; Score 307; DB 54; Length 333;
Best Local Similarity 96.1%; Pred. No. 1.25e-297;
Matches 320; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 1 gacattgtctgacagctctctgtcttcttagctgtatctctggggcagagggccacc 60
Qy 61 GACATTGTGCTGACAGCTCTCCTGTTCTTAGGTGTATCTCTGGGGCAGAGGGCCACC 120
Db 61 atctcatcagggccagcaaaagtctcagtagcatctcgtgctatgttatgtcactggtac 120
Qy 121 ATCTCATCAGGGCCAGCAAAAGTCTGCTAGCATCTGGCTATGTATATCATCGTGTAC 180
Db 121 caacagaacacagcagcagcccaacctctcatctatctttgtcaccacctaatact 180
Qy 181 CAACAGAACACGAGCAGACACCAAACTCCTCATCTATCTTCATCCACCTAGAACTCT 240

Jul 8 08:22

US-08-137-117B-24.fge

12

Db 181 ggggtccctgcaggttcagtgccagtggtgggtctgggacagacttcacccctcaacatccat 240
Qy 241 GGGGTCCCTGCCAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCTCAACATCCAT 300
Db 241 cctgtggagaggaggtcgtgcaacctattactgtcagcacagtagtagggaggttcctccg 300
Qy 301 CCTGTGGAGGAGGAGGATGCTGCACCTATTACTGTGACGACAGTAGGAGAATCCGTAC 360
Db 301 acgttcgggtggagcaccagagctggaataaaa 333
Qy 361 ACCTTCGGAGGGGGACCAAGCTGGAATAAAA 393

RESULT 9
LOCUS MMIGVK20P 690 bp DNA ROD 17-FEB-1995
DEFINITION M.musculus Ig Vkappa-pseudo-HNK20 gene.
ACCESSION X82689
KEYWORDS immunoglobulin; kappa light chain; pseudogene; variable region.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorphia; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 690)
AUTHORS Berdoz, J. and Kraehenbuhl, J.P.
TITLE Specific amplification by the polymerase chain reaction of rearranged genomic variable regions of immunoglobulin genes from mouse hybridoma cells

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 690)
AUTHORS Berdoz J.A.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1994) to the EMBL/GenBank/DBJ databases. J.A. Berdoz, Swiss Institute for Experimental Cancer Research, 155 ch. des Boveresses, 1066 Epalinges, SWITZERLAND

COMMENT NCBI gi: 673445
FEATURES
Location/Qualifiers
source
1..690
/organism="Mus musculus"
/rearranged
/cell_type="hybridoma cell"
/cell_line="HNK20"
1..65
/number=1
join(1..65,304..>647)
1..25
join(26..65,304..314)
/genes="Ig Vkappa-HNK20"
join(26..65,304..>647)
/genes="Ig Vkappa-HNK20"

exon
1..65
/number=1
mRNA
5'UTR
sig_peptide
CDS
intron
66..303
/number=1
304..647
/number=2
315..647
mat_peptide
/product="variable region of the Ig kappa light chain"
648..690
intron
/number=2
BASE COUNT 171 a 169 c 155 g 195 t
ORIGIN

sig_peptide	61..109 /notes="Ig kappa V-region 1.5kb-V-kappa signal peptide" /codon_start=1
exon	61..109 /notes="Ig kappa V-region 1.5kb-V-kappa, exon 1; putative" join(61..109,351..361)
sig_peptide	/notes="Ig kappa V-region 1.5kb-V-kappa signal peptide" /codon_start=1
intron	110..350 /notes="VK1.5 intron A" 351..658
exon	/notes="Ig kappa V-region 1.5kb-V-kappa, exon 2; putative" 351..361
sig_peptide	/notes="Ig kappa V-region 1.5kb-V-kappa signal peptide" /codon_start=1
exon	351..>659 /notes="Ig kappa V-region 1.5kb-V-kappa" /number=2
exon	351..361 /notes="Ig kappa V-region 1.5kb-V-kappa signal peptide, exon 2; putative"
mat_peptide	362..659 /partial /notes="Ig kappa V-region 1.5kb-V-kappa mature peptide" /codon_start=1
idNA	660..>706 /notes="V-J intervening DNA (5' end +/- 1 bp)"

BASE COUNT	175 a	178 c	156 g	197 t
ORIGIN	1 bp upstream of EcoRI site on chromosome 6.			
Query Match	77.6%; Score 305; DB 56; Length 706;			
Best Local Similarity	98.7%; Pred. No. 2.07e-295;			
Matches	309; Conservative	0; Mismatches	4; Indels	0; Caps 0;

Db	345	t t c c a g g t t c c a a c t g g t g a c a t t g t g t c a c a c a g t c t c t g c t t c c t t a g t g t a t c t c	404
Qy	44	T T C C A G G T T C C A C T T G G T G A C A T T G C T G C T C A C A G A G T C T C T G C T T C C T T A G G T G A T A T C T	103
Db	405	t g g g c c a g a g g c c a c a t c t c a t g c a g g c c a g a a a a g t g c a g t a c a t c t g c t a t a	464
Qy	104	T G G G C A G A G G G C C A C A T C A T C A T G C A G G G C C A G A A A A G T G C A G T A C A T C T G G C T A T A	163
Db	465	g t a t a t g c a c t g g t a c a a c a g a a a c a g g a c a g c a c c a a a c t c c t c a t c a t c t g	524
Qy	164	G T T A T A T G C A C T G T C A C C A G A A A C A G G A C A G A C C C A A A A C T C C T C A T C T A T C T T G	223
Db	525	c a t c a a c c t a g a a t c g g g t c c c t g c c a g g t t c a g t g c a g t g g g t c t g g g a c a c t	584
Qy	224	C A T C C A A C C T A G A A T C T G G G T C C C T G C C A G T T C A G T G G C A G T G G G T T G G G A C A C A C T	283
Db	585	t c a c c c t c a a c a t c a t c c t g t g g a g a g a g g a t g c t c a a c c t a t t a c t g t c a g c a c a	644
Qy	284	T C A C C C T C A C A T C C A T C C T G T G A G A G A G G A T G C T C A A C C T A T T A T G T C A G C A C A	343
Db	645	g t a g g a g c t t c c	657
Qy	344	G T A G G G A G A A T C C	356
RESULT	11		
LOCUS		WMJG21F5	666 bp DNA
			04-AUG-1992

RESULT	11			
LOCUS	MM1G21E5	666 bp	DNA	ROD
				04-AUG-1992

Jul 8 08:22

US-08-137-117B-24.rge

15

```
DEFINITION Mouse Ig light chain V(kappa)2IE-J(kappa)5 rearranged DNA,
non-functional.
ACCESSION X13938 Y00804
KEYWORDS Ig kappa light chain; Ig light chain; immunoglobulin; pseudogene;
rearranged DNA; variable region.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 666)
AUTHORS Mueller, B.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-1989) to the EMBL/GenBank/DBJ databases. Mueller
B., Institut fuer Genetik, Weyertal 121, 5000 Koeln 41, FRG
REFERENCE 2 (bases 466 to 666)
AUTHORS Muller, B. and Reth, M.
TITLE Ordered activation of the Ig lambda locus in Abelson B cell lines
JOURNAL J. Exp. Med. 168 (6), 2131-2137 (1988)
MEDLINE 89067821
COMMENT the correctly rearranged V(kappa)2IE segment is not functional
because it carries a 1-bp deletion in the leader sequence Data kindly
reviewed (28-NOV-1990) by Mueller B.
FEATURES
source
location/Qualifiers
1..666
/organism="Mus musculus"
/strain="NIH/3T3"
/cell_line="B1p8-7b Abelson 300-19"
/chromosome="6"
misc_feature 60..107
/note="V(kappa)2IE leader"
misc_feature 341..646
/note="V(kappa)2IE exon"
misc_feature 647..666
/note="J(kappa)5 region"
BASE COUNT 160 a 167 c 151 g 188 t
ORIGIN
Query Match 77.1%; Score 303; DB 53; Length 666;
Best Local Similarity 98.4%; Pred. No. 3.42e-293;
Matches 308; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 335 ttccaggtccactggagacattgtgtgcacagtcctctgttccctagctgtatctc 394
|||||
Qy 44 TTCAGGTTCCACTGGTGACATTGCTGTGACACAGTCCTCTCTTCTAGGTGTATCTC 103
|||||
Db 395 tggggcagagggccaccatctcatgcaggccagcaaaagtgtcagcatctggctata 454
|||||
Qy 104 TGGGCGACAGGGCCACCATTCTCATGACGGGCGAGCAAAAGTGTCACTATCTGGCTATA 163
|||||
Db 455 gttatatgactggtaccacagaaccaggacagccaccaactcctcatctctcttg 514
|||||
Qy 164 GTTATATGCACTGGTACCAACAGAACCCAGGACAGACACCCCAACTCTCATCTCTTG 223
|||||
Db 515 catccaacctagaaactctgggtccctgccaggttcagtgccagtggtctggagacagact 574
|||||
Qy 224 CATCAACACTAGAAATCGGGGTCCTCGCCAGGTTTCAGTTCAGTGGGCTGGGACAGACT 283
|||||
Db 575 tcacctcaacatccatcctgtggaggaggaggtgtgcaacctattactgtcagcaca 634
|||||
```

Jul 8 08:22

US-08-137-117B-24.rge

16

```
Qy 284 TACCCCTCAACATCCATCTCTGTGGAGGAGGAGATGCTGCAACCTATTACTGTGACACA 343
|||||
Db 635 gtaggagctctcc 647
|||||
Qy 344 GTAGGAGAAATCC 356
|||||
RESULT 12
LOCUS MDICKVBI 333 bp RNA ROD 05-NOV-1994
DEFINITION M.domesticus Igk variable region.
ACCESSION Z22098
KEYWORDS anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 333)
AUTHORS Tillman, D.M., Jou, N.T., Hill, R.J. and Marion, T.N.
TITLE Both IgM and IgG anti-DNA antibodies are the products of clonally
selective B cell stimulation in (NZB x NZW)F1 mice
JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)
MEDLINE 92381444
REFERENCE 2 (bases 1 to 333)
AUTHORS Marion, T.N.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-1993) to the EMBL/GenBank/DBJ databases. Tony N.
Marion, Microbiology and Immunology, University of, Tennessee,
Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA
NCBI gi: 297663
FEATURES
source
location/Qualifiers
1..333
/organism="Mus domesticus"
/strain="(NZB x NZW)F1"
/dev_stage="somatic variant"
/tissue_type="spleen"
/cell_type="hybridoma"
/cell_line="17s.16"
/isolate="mouse #17"
/chromosome="6"
/sex="Female"
<1..>333
/genes="Igk"
/notes="17s.16 is clonally related to the IgG hybridomas
17s.94 and 17s.124 in clone 17s-c4. NCBI gi: 297664"
/codon_start=1
/function="kappa light chain variable region for anti-DNA
antibody; Vk21 family"
/product="immunoglobulin variable region"
/translation="DIVLTQSPASLAVSIGQRATISCRASQSVSTAYSITHWYQKP
QQTPELLIKYASNLDSGVPARFSCSGTDFTNHPVEEDTATYYCQHSWEIPFTF
GGTKLEIK"
BASE COUNT 88 a 87 c 82 g 75 t 1 others
ORIGIN
Query Match 76.6%; Score 301; DB 53; Length 333;
Best Local Similarity 94.9%; Pred. No. 5.65e-291;
Matches 316; Conservative 1; Mismatches 16; Indels 0; Gaps 0;
Db 1 gacattgtctacacagtctctgtctcttagctgtatctctgtgggagggccacc 60
|||||
```



```
exon          1..49
              /number=1
              /product="partial signal peptide"
CDS            1..394
              /partial
              /note="V gene is identical to VK21c germline gene; uses
              JK1; NCBI gi: 403072"
              /codon_start=1
              /product="Ig variable region, light chain"
              /translation="METDTLLIWLWVPGTGDIVLTQSPASIVSLQRATISGR
              ASEVSDYNGNSPMHWYQOKPQPKLIVRASNLSEGPAREPGSGSRDTDFLTINPV
              EADVATVYQQSNEDRPTFGGKLEIK"
              50..394
exon           /number=2
              /product="carboxyl end of signal peptide and mature heavy
              chain"
              61..135
misc_feature   /standard_name="FR1"
              61..393
mat_peptide    /product="Ig variable region, light chain"
              136..168
misc_feature   /standard_name="CDR1"
              169..219
misc_feature   /standard_name="FR2"
              220..228
misc_feature   /standard_name="CDR2"
              229..339
misc_feature   /standard_name="FR3"
              340..357
misc_feature   /standard_name="CDR3"
              358..393
              /standard_name="FR4"
BASE COUNT    99 a 100 c 98 g 97 t
ORIGIN
Query Match   76.1%; Score 299; DB 54; Length 394;
Best Local Similarity 88.0%; Pred. No. 9.33e-289;
Matches 346; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Db 1 atggagacagacactcgtgtatgggtactgctgctgggtccaggttccactggt 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 ATGGAGTCACACACACTCCTCTATGGGTACTGCTGCTGGGTCCAGGTCCACTGGT 60

Db 61 gacattgtgctaacaacatctccagctctcttggctgtgtctctaggcagagggccacc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GACATTGTGTCACAGCTCTCCTGCTTAGGTGTATCTCTGGGCGAGGGCCACC 120

Db 121 atatcctgcagagcagtgaaagtgtgatagttatggcaatagtttttactgcactggtac 180
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 ATCTCATCGAGGCGCAGCAAAAGTGTGAGTACATCTGGCTATAGTTATATGCACCTGGTAC 180

Db 181 cagcaagaaccagcagcagccaccacaaacctctcatctatcgtgtcatccaacctagaatct 240
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 CACAGAACCCAGCAGACAGACACCAACTCTCTCATCTATCTTGCAATCCAACTAGAACT 240

Db 241 gggatccctgccagggttcagtgccagtggtgggtcaggacagacttcaccctaccatatt 300
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 GGGGTCCCTGCCAGGTTTCAGTGTGGCAGTGGGTCTGGGACAGACTTCACCTCCATCATCAT 300

Db 301 cctgtggaggtgatgatgttgcaacctattactgtcagcaaaagttaatgaagatcctcgg 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 CCTGTGGAGGAGGAGGATGCTGCAACTATTACTGTCCAGCACAGTAGGAGAGATCCGTAC 360

Db 361 acgttcogtggaggccaccaagctggaaatcaaa 393
```

```
||||| || || ||||| ||||| ||||| |||||
QY 361 ACGTTGGAGGGGGACCAAGCTGGAAATAAAA 393

RESULT 15
LOCUS      MUSIGKAAS 339 bp mRNA 30-JUN-1987
DEFINITION Mouse immunoglobulin aberrantly rearranged kappa-chain mRNA
ACCESSION MI4435
KEYWORDS   V138J2-region from hybridoma CEA 66-E3.
           C-region; J-region; V-region; immunoglobulin-kappa;
           processed gene; pseudogene.
SOURCE     Mouse hybridoma CEA 66-E3, cDNA to mRNA.
ORGANISM   Mus musculus
            Eukaryota; Amalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 339)
AUTHORS   Cabilly,S. and Riggs,A.D.
TITLE     Immunoglobulin transcripts and molecular history of a hybridoma
           that produces antibody to carcinoembryonic antigen
JOURNAL    Gene 40, 157-161 (1985)
MEDLINE    86137415
COMMENT    A 4 nt deletion at the V-J recombination site causes misalignment
           of the V and J segments resulting in a nonfunctional kappa-chain.

FEATURES             Location/Qualifiers
     source            1..339
                        /organism="Mus musculus"
     sig_peptide       <1..6
                        /note="pseudo-Igk leader pept"
     CDS               /pseudo
                        /codon_start=1
                        <1..>339
                        /note="pseudo-Igk precursor"
     mat_peptide       7..>339
                        /note="pseudo-Igk"
                        /codon_start=1
BASE COUNT    87 a 90 c 86 g 76 t
ORIGIN         Chromosome 6.

Query Match       75.3%; Score 296; DB 56; Length 339;
Best Local Similarity 95.9%; Pred. No. 1.97e-285;
Matches 325; Conservative 0; Mismatches 11; Indels 3; Gaps 2;

Db 1 actggtgacattgctgacagctctcctgctccttagctgtatctctgtggggcagagg 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 55 ACTGCTGACATTGTTGCTGACAGCTCTCTGCTTCTTAGTGTATCTCTGGGCGACAGG 114

Db 61 gccacctctatacaggccagcaaaagtgcagtacatctggctatagtatatgcac 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 115 GCCACCTCTCATCGAGGCCAGCCAAAAGTGCAGTACATCTGGCTAGTTATATGCAC 174

Db 121 tggaaaccaagaaccaggacagccaccgaactcctcatctatctgtatccaaccta 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 TGGTACCAACAGAACCCAGCAGACACCCAACTCTCATCTATCTTGCATCCAACCTA 234

Db 181 gaatctgggtccctgccaggttcagtgccagtggtcctgggacagacttcaccctcaac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 GAATCTGGGTCCCTGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACCCCTAAC 294

Db 241 atccatcctgtgaggaggagatgctgcaacctattactgtcagcacattagg-gag- 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

21

Qy 355 CCGTACACGTTCCGAGGGGGACCAAGCTGGAAATAAAA 393

Search completed: Mon Jul 8 08:33:17 1996
Job time : 351 secs.

Jul 8 08:27

US-08-137-117B-24.rst

1

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPerch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Mon Jul 8 08:34:42 1996; MasPar time 182.60 Seconds
773.735 Million cell updates/sec
Tabular output not generated.

Title: >US-08-137-117B-24
Description: (1-393) from US08137117B.seq
Perfect Score: 393
N.A. Sequence: 1 ATGAGTGTGACACACTCTCT.....GGACCAAGCTGGAATAAAA 393
Comp: TACCTAGTCTGTGTGAGCA.....CTGGTTCACCTTATTTT

Scoring table:
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:
EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94
EST-STS-TWO
95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5
100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10
105:gnEST11 106:gnEST12 107:gnEST13 108:gnEST14 109:gnEST15
110:gnEST16 111:gnEST17 112:gnEST18 113:gnEST19 114:gnEST20
115:gnEST21 116:gnEST22 117:gnEST23 118:gnEST24 119:gnEST25
120:gnEST26 121:gnEST27 122:gnEST28 123:gnEST29
124:gnEST30 125:gnEST31 126:gnEST32 127:gnEST33

Database:

Jul 8 08:27

US-08-137-117B-24.rst

2

128:enEST20 129:enEST21 130:enEST1 131:enSTS2 132:enSTS3

Statistics: Mean 10.000; Variance 1.898; scale 5.268

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	123	31.3	488	11	H25625	y148g05.rl	Homo sapiens	4.04e-198
2	105	26.7	467	12	H27034	y165d05.rl	Homo sapiens	1.74e-160
3	104	26.5	364	127	HST27579	EST100049	Homo sapiens	2.06e-158
4	104	26.5	364	69	T27579	EST100049	Homo sapiens	2.06e-158
5	93	23.7	470	114	HS115213	yu40h01.rl	Homo sapiens	9.43e-136
6	93	23.7	470	97	H62115	yu40h01.rl	Homo sapiens	9.43e-136
7	92	23.4	359	127	HST27587	EST100475	Homo sapiens	1.05e-133
8	92	23.4	359	69	T27587	EST100475	Homo sapiens	1.05e-133
9	88	22.4	357	70	T29104	EST69270	Homo sapiens	1.50e-125
10	88	22.4	357	114	HS10412	EST69270	Homo sapiens	1.50e-125
11	86	21.9	445	47	R48141	yj66c09.rl	Homo sapiens	1.72e-121
12	85	21.6	381	114	HS11411	EST69430	Homo sapiens	1.83e-119
13	85	21.6	381	70	T29114	EST69430	Homo sapiens	1.83e-119
14	85	21.6	430	115	HS156227	yf86f06.rl	Homo sapiens	1.83e-119
15	85	21.6	430	98	H69156	yf86f06.rl	Homo sapiens	1.83e-119
16	84	21.4	503	41	R28232	yh57e08.rl	Homo sapiens	1.93e-117
17	83	21.1	383	70	T29916	EST99871	Homo sapiens	2.02e-115
18	83	21.1	383	125	HS91615	EST99871	Homo sapiens	2.02e-115
19	83	21.1	463	53	R69532	yj82d09.rl	Homo sapiens	2.02e-115
20	82	20.9	383	69	T27870	EST19007	Homo sapiens	2.09e-113
21	82	20.9	383	127	HST27870	EST19007	Homo sapiens	2.09e-113
22	77	19.6	210	53	R69482	yj83c03.rl	Homo sapiens	2.24e-103
23	77	19.6	393	69	T27593	EST100653	Homo sapiens	2.24e-103
24	77	19.6	393	127	HST27593	EST100653	Homo sapiens	2.24e-103
25	76	19.3	332	118	HS34210	EST77181	Homo sapiens	2.22e-101
26	76	19.3	332	70	T29342	EST77181	Homo sapiens	2.22e-101
27	76	19.3	390	17	H45841	yp22b04.rl	Homo sapiens	2.22e-101
28	76	19.3	390	124	HS841242	yp22b04.rl	Homo sapiens	2.22e-101
29	76	19.3	438	51	R64693	yj22f09.rl	Homo sapiens	2.22e-101
30	75	19.1	434	87	T93178	ye24e07.rl	Homo sapiens	2.17e-99
31	73	18.6	203	15	H39743	yo53d07.rl	Homo sapiens	2.03e-95
32	73	18.6	279	70	T29656	EST89211	Homo sapiens	2.03e-95
33	73	18.6	279	122	HS65610	EST89211	Homo sapiens	2.03e-95
34	73	18.6	516	52	R67559	yi42h11.rl	Homo sapiens	2.03e-95
35	69	17.6	359	12	H27642	yj61g07.rl	Homo sapiens	1.58e-87
36	68	17.3	408	58	R86035	yp12g07.rl	Homo sapiens	1.44e-85
37	68	17.3	451	86	T90236	ye15d10.rl	Homo sapiens	1.44e-85
38	66	16.8	257	48	R51193	yj71a07.rl	Homo sapiens	1.17e-81
39	66	16.8	397	47	R49771	yj55c03.rl	Homo sapiens	1.17e-81
40	65	16.5	261	46	R46878	yj54h03.rl	Homo sapiens	1.03e-79
41	64	16.3	570	53	R70290	yj81d08.rl	Homo sapiens	8.98e-78
42	63	16.0	360	56	R79907	yj85f01.rl	Homo sapiens	7.74e-76
43	63	16.0	395	70	T29112	EST69384	Homo sapiens	7.74e-76
44	63	16.0	395	114	HS11211	EST69384	Homo sapiens	7.74e-76
45	62	15.8	141	15	H39551	y167h12.rl	Homo sapiens	6.59e-74

ALIGNMENTS

RESULT 1 H25625 488 bp mRNA EST 10-JUL-1995
LOCUS

Jul 8 08:27

US-08-137-117B-24.rs

3

DEFINITION y148g05.r1 Homo sapiens cDNA clone 161528 5' similar to gb:X72467
IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);.

ACCESSION
H25625
KEYWORDS
SOURCE

human clone=161528 library=Soares breast 3NbHBst vector=pf7T3D
(Pharmacia) with a modified polylinker host=DHI08 (ampicillin
resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified p7T3 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 488)

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 362

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 894748

FEATURES

source

Location/Qualifiers

1..488

/organism="Homo sapiens"

/clone="161528"

/note="human"

BASE COUNT 99 a 130 c 128 g 127 t 4 others

ORIGIN

Query Match 31.3%; Score 123; DB 11; Length 488;

Best Local Similarity 68.0%; Pred. No. 4.04e-198;

Matches 257; Conservative 0; Mismatches 118; Indels 3; Gaps 3;

Db 21 ctctcggggctgaatgctctggtctctggtccagtgaggatattgtgatctcag 80

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 19 CTCTATGGGTACTGCTGCTGGGTTCCAGTTCCATGCTGACATTGCTGCACACAG 78

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 81 tctccactctccagccgctaccctggagcggcgtccactctctcgaagttagt 140

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 79 TCTCTGCTTCTTAGGTGTAATCTCTGGGGCAGAGGGCCACCATCTGCAGGGCCACC 138

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 141 cagagcctctacatgaatgatacagatttttgattggtacctcgagaagccagga 200

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 139 AANAAGTGTCAGT-ACA-TC-TGGCTATAGTTATATGCACTGCTGACCAAGAACACGGA 195

Jul 8 08:27

US-08-137-117B-24.rs

4

Db 201 cagttctccacagctctgatctattgttttaagcggcctccgggtccctgacag 260

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 196 CAGACACCCAAATCCTCATCTATCTTGATCCAACTAGAAATCTGGGGTCCCTGCCAGG 255

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 261 ttcaagtgcagtgatcagggcacagattttacaactgagaatcagtagtgagctgag 320

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 256 TTCAGTGGCAGTGGGCTCGGACAGACTTCACCCCTCAACATCCATCTCTGGAGGAGGAG 315

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 321 gatgttggtcttttattactgcataaaactctacagaccccgctcacttttcgcggaggg 380

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 316 GATGCTGCACACCTATTACTGACGACAGTAGGAGAAATCCGTACACGTTTCGGAGGGGGG 375

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 381 accaaggttagatncaa 398

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 376 ACCAAGCTGCAAAATAAAA 393

||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2

LOCUS H27034 467 bp mRNA EST 12-JUL-1995

DEFINITION y16505.r1 Homo sapiens cDNA clone 163113 5' similar to gb:X72467

IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);.

ACCESSION H27034

KEYWORDS EST.

SOURCE human clone=163113 library=Soares breast 3NbHBst vector=pf7T3D

(Pharmacia) with a modified polylinker host=DHI08 (ampicillin

resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Adult human.

1st strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTACCAATCTGAAGTGGGAGCGGCCCTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),

digested with Not I and cloned into the Not I and Eco RI sites of a

modified pf7T3 vector (Pharmacia). Library went through one round

of normalization to a Cot = 20. Library constructed by Bento Soares

and M.Fatima Bonaldo.

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 467)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 352

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 897024

Location/Qualifiers

1..467

/organism="Homo sapiens"

FEATURES

source

TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pTT3 vector (Pharmacia). Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 470)

AUTHORS

Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Ruhlberg, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.edu

High quality sequence stops: 354

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 1014947

FEATURES

Location/Qualifiers

source

1..470

/organism="Homo sapiens"

/clone="236305"

mRNA

<1..>470

BASE COUNT

112 a 108 c 119 g 120 t 11 others

ORIGIN

Query Match

Best Local Similarity 23.7%; Score 93; DB 97; Length 470;

Matches 160; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Db

19 tatttngactggtaactgcagaagccaggcgagtcacacagtcctgatatacgtt 78

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy

166 TATATGCAGCTGTACACAGACAAACACGACAGACACCAACTCTATCTATCTGCA 225

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db

79 tctatcgccctctgcagtcaccagacaggttcagtgccagtggtgcagcactgattc 138

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy

226 TCACACTAGATCTGTGGGTCCTCGCAGGTCAGTGGCAGTGGGCTGGGACAGACTTC 285

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db

139 acaactgaaatcagcaggggtggaggctgagatgttgaggattattactgcagcaagct 198

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy

286 ACCCTCAACATCCATCTCTGTGGAGGAGGAGATGCTGCAACCTATTACTGACGACAGT 345

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db

199 atagagtttcttggaacttttggccaggggacccaagctggagatcaaa 246

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy

346 AGCGAATCCGTACACCTCGGAGGGGGACCAAGCTCGAATAAATA 393

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT

7

ID

HST27587

AC

T27587; standard; RNA; EST; 359 BP.

DT 12-JAN-1995 (Rel. 42, Created)
DT 07-SEP-1995 (Rel. 45, Last updated, Version 2)
DE EST100475 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
light chain V region (GB:X63397) (HT:3865).
KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

RN [1]

RP 1-359

RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

RA Bult C.J., Iee N., Kirkness E.F., Weinstein K.G., Gocayne J.D.,

RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,

RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,

RA FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geohagen N.S.M.,

RA Glodok A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,

RA Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,

RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,

RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,

RA Weidman J.F., Li Y., Bedharik D.P., Cao L., Cepeda M.A.,

RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferris A.,

RA Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,

RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,

RA Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,

RA Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,

RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;

RT *Initial Assessment of Human Gene Diversity and Expression

Patterns Based Upon 52 Million Basepairs of cDNA Sequence";

RL Unpublished.

CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper

CC Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:

CC tdbinfo@db.tigr.org For clone availability, additional sequence

CC and expression information related to this EST, please contact the

CC TIGR Database (tdbinfo@db.tigr.org). NCBI gi: 609685

Key Location/Qualifiers

FT source

1..359

/organism="Homo sapiens"

/note="human"

FT mRNA

<1..>359

SQ Sequence 359 BP; 75 A; 93 C; 95 G; 94 T; 2 other;

Query Match

Best Local Similarity 23.4%; Score 92; DB 127; Length 359;

Matches 207; Conservative 0; Mismatches 93; Indels 4; Gaps 4;

Db

25 ctctctggggctgaatgctctgggtctctggagccgagcgccctttatctcctcaggtctagt 144

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy

19 CTGCTATGGGTACTGCTGCTGGGTTCCAGGTTCCACTGCTGCATCTGCTGCACAG 78

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db

85 tctcactctcctgccgtaccctccctggagagcgccctttatctcctcaggtctagt 144

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy

79 TCTCTCTCTTCTTAGGTGTATCTGTGGGCGAGGGCCACCATCTCATCGAGGCCAGC 138

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db

145 cagagactcctgactgactggacacaactatttggattggattgacgaagcgaagg 204

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy

139 AAAAGTCTCA-GTACA-T-CTGGCTATAGTTATATGCACCTGGTACCAACAGAAACAGGA 195

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db

205 cagctctccacaactcctgatctatttgggttctaatacgggcctccgggttccctgacagg 264

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy

196 CAGACACCCAAACTCCTCATCTATCTTTCATCCAACTAGAAATCTGGGGTCCCTGCCAGG 255

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db

265 ttcagtggcagtggggatcaggcagcagattttacactgaaataaagcagagatggaggtga 324

Jul 8 08:27

US-08-137-117B-24.rst

11

QY 256 TTACGTGGCAGTGGG-TCTGGGACAGACTTCACCCCTCAACATCCATCTCTGTGGAGGAGGA 314
|||||
Db 325 ggat 328
|||||
QY 315 GGAT 318
|||||

RESULT 8
LOCUS T27587 359 bp mRNA EST 06-SEP-1995
DEFINITION EST100475 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
light chain V region (GB:X63397) (HT:3865).
ACCESSION T27587
KEYWORDS EST.
SOURCE human primer=M13 Reverse library=Human Pancreas.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 359)

REFERENCE
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S.,
Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palancques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,
Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
Haseitine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

COMMENT
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org).

FEATURES
source NCBI gi: 609685
Location/Qualifiers
1..359
/organism="Homo sapiens"
/note="human"
mRNA 75 a 93 c 95 g 94 t 2 others
BASE COUNT <1..>359
ORIGIN

Query Match 23.4%; Score 92; DB 69; Length 359;
Best Local Similarity 68.1%; Pred. No. 1.05e-133;
Matches 207; Conservative 0; Mismatches 93; Indels 4; Gaps 4;

Jul 8 08:27

US-08-137-117B-24.rst

12

Db 25 ctccctggggctgctaagtctctgggtctctggatccagtggggtattgttctgactcag 84
|||||
QY 19 CTGCTATGGGTACTGCTGCTGTGGGTTCCAGGTTCCACTGGTGACATTGGTGTGACACAG 78
|||||

Db 85 tctccactctccctgccqgnhacccctggagagcggcctttatctctgcaggtctagt 144
|||||
QY 79 TCTCCTGCTTCCTTAGTGTATCTCTGGGGCAGAGGGCCACCATCTCATCGAGGGCCAGC 138
|||||

Db 145 cagagactctcgtactgtagcacacaactatttggttgacctgcagaagccagg 204
|||||
QY 139 AAGAGTCTCA-GTACA-TCTGGCTATAGTTATGCACTGGTGTACCAACAGAAACACGGA 195
|||||

Db 205 cagtcctccaaactcctgatctatttggttctaatcgggcctcgggggtccctgcagcagg 264
|||||
QY 196 CAGACACCCAAATCCTCATCTATTGTCATCCAACTAGAAATCTGGGGTCCCTGCCAGG 255
|||||

Db 265 ttccagtgccagtgggatccagcacagattttacactgaaataaagcagagtgaggctga 324
|||||

QY 256 TTCAGTGGCAGTGGG-TCTGGGACAGACTTCACCCCTCAACATCCATCCTCTGGAGGAGGA 314
|||||

Db 325 ggat 328
|||||
QY 315 GGAT 318
|||||

RESULT 9
LOCUS T29104 357 bp mRNA EST 06-SEP-1995
DEFINITION EST69270 Homo sapiens cDNA 5' end similar to immunoglobulin kappa
light chain V region (GB:X54248) (HT:3095).
ACCESSION T29104
KEYWORDS EST.
SOURCE human primer=M13 Reverse library=Human Lymphoid tissue.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 357)

REFERENCE
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W.,
Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S.,
Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M.,
Merrick,J.M., Moreno-Palancques,R.F., McDonald,L.A., Nguyen,D.T.,
Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R.,
Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H.,
Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
Haseitine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)
Other_ESTs: EST69269
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056

TITLE
JOURNAL
COMMENT

RA Kelley J.M., Klymek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

SOURCE human clone=153712 library=Soares breast 2NbHBst vector=pT7

[illegible]

студент А., имени С.Д.; наша М.С.; посетил Б.,
Колле Т.М. К.И.-К.М. К.-К.М. К.-К.М. К.-К.М.

Имя	Отчество	Пол	Возраст	Стаж	Средняя зарплата	Средняя зарплата в % к средней по району
Иванов	И.И.	М	45	10	1200	100
Петров	П.П.	М	50	15	1100	92
Сидоров	С.С.	М	40	8	1300	108
Климов	К.К.	М	55	20	1050	88
Васильев	В.В.	М	48	12	1150	96
Попов	П.П.	М	52	18	1080	90
Смирнов	С.С.	М	42	9	1250	104
Михайлов	М.М.	М	58	22	1020	85
Кузнецов	К.К.	М	47	11	1180	98
Лебедев	Л.Л.	М	53	19	1060	89
Зинченко	З.З.	М	43	7	1280	106
Березин	Б.Б.	М	57	21	1040	87
Воробьев	В.В.	М	46	10	1190	99
Григорьев	Г.Г.	М	51	16	1090	91
Давыдов	Д.Д.	М	44	9	1220	102
Исупов	И.И.	М	54	17	1070	89
Колесников	К.К.	М	41	6	1320	110
Лавров	Л.Л.	М	56	20	1030	86
Морозов	М.М.	М	49	11	1170	97
Новиков	Н.Н.	М	59	23	1010	84
Осипов	О.О.	М	46	10	1210	101
Романов	Р.Р.	М	50	15	1110	93
Соловьев	С.С.	М	40	8	1310	109
Тихонов	Т.Т.	М	55	20	1050	88
Федотов	Ф.Ф.	М	47	11	1180	98
Харьков	Х.Х.	М	52	18	1080	90
Цыганов	Ц.Ц.	М	43	7	1280	106
Чайков	Ч.Ч.	М	57	21	1040	87
Шаров	Ш.Ш.	М	46	10	1190	99
Шевченко	Ш.Ш.	М	51	16	1090	91
Щербинин	Щ.Щ.	М	44	9	1220	102
Юрьев	Ю.Ю.	М	54	17	1070	89
Яковлев	Я.Я.	М	41	6	1320	110

AGACACCCAACTCCTCATCTATCTTGCACTCAACCTAGAATCTGGGTCCC

Db 292 catcagacttgaacctgaagattttacac

[illegible]

Jul 8 08:27

US-08-137-117B-24.rst

19

QY 196 CAGACACCAAACTCCTCATCTATCTTCGATCCAACTAGATCTGGGGTCCCTGCCAGG 255

Db 264 ttcaatggcagtgnggcaggagcagatttcacact 298

QY 256 TTCAGTGGCAGTGGGTCTGGGCAGACACTTCACCCCT 290

RESULT 15

LOCUS H69156 430 bp mRNA EST 19-OCT-1995

DEFINITION yr86f06.r1 Homo sapiens cDNA clone 212195 5' similar to

gb:XS5400_cdel IG KAPPA CHAIN PRECURSOR V-II REGION

(HUMAN); contains Alu repetitive element;.

ACCESSION H69156

KEYWORDS EST.

SOURCE

human clone=212195 primer=M13R1 library=Soares fetal liver spleen

INFLS vector=p7T73D (Pharmacia) with a modified polylinker

host=DH10B (ampicillin resistant) Rsite1=Pac I Reite2=Eco RI Liver

and spleen from a 20 week-post conception male fetus. 1st strand

cDNA was primed with a Pac I - oligo(dT) primer [5'

AACTGCAAGATTAAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded

cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac

I and cloned into the Pac I and Eco RI sites of the modified p7T73

vector. Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;

Sarcopterygii; Choonata; Tetrapoda; Amniota; Mammalia; Theria;

Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfling,T., Soares,M., Tan,F.,

Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 267

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 1030482

FEATURES Location/Qualifiers

source

1..430

/organism="Homo sapiens"

/clone="212195"

/note="human"

mRNA <1..>430

BASE COUNT

98 a 107 c 116 g 101 t 8 others

ORIGIN

Query Match

Best Local Similarity 21.6%; Score 85; DB 98; Length 430;

Matches 187; Conservative 0; Mismatches 85; Indels 3; Gaps 3;

Jul 8 08:27

US-08-137-117B-24.rst

20

Db 24 cttctggggctgctaatgctctggtccctggatccagtggggataattgtgatgccacag 83

QY 19 CTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGACATTGTGCTGACACAG 78

Db 84 actccactctcctcaccctgtcaacccttgagacagcggcctccatctcctgcaggtctagt 143

QY 79 TCTCCTGCTTCTTGGTGTATCTCTGGGGCAGAGGGCCACCATCTCATCGAGGGCCAGC 138

Db 144 caaagcctctacacagtgatggaacacactacttgagttggcttcagcagagggccaggc 203

QY 139 AAAAGTCTCAGT-ACA-TC-TGGCTATAGTTATATGCACTGGTACCAACAGAAACAGGA 195

Db 204 cagcctccaagactcctcaattataagatttctaaccgggttctctctgggggtccccagacaga 263

QY 196 CAGACACCAAACTCCTCATCTATCTTGCATCCAACTAGATAATCTGGGGTCCCTGCCAGG 255

Db 264 ttcaatggcagtgnggcaggagcagatttcacact 298

QY 256 TTCAGTGGCAGTGGGTCTGGGCAGACACTTCACCCCT 290

Search completed: Mon Jul 8 08:38:06 1996

Job time : 204 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPsrch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:28:23 1996; MasPar time 7.40 Seconds
447.403 Million cell updates/sec

Tabular output not generated.

Title:	>US-08-137-117B-25
Description:	(1-131) from US08137117B.pep

94Z
 1 MESDTLLLVLLWVPGSTG.....CQHSRENPTFGGGTKLEIK 131

Scoring table: PAM 150
Gap 11

Searched: 82306 seqs, 25270970 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

pir46

1:ann1 2:ann2 3:ann3 4:unann1 5:unann2 6:unann3 7:unann4
8:unann5 9:unann6 10:unann7 11:unann8 12:unrev1
13:unrev2

Statistics: Mean 41.173: Variance 148.737: scale 0.277

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description	Pred. No.
		Match						
1	859	91.2	131	13	S55027		immunoglobulin light	2.53e-81
2	837	88.9	140	5	PN0446		Ig kappa chain precu	8.94e-79
3	819	86.9	131	2	KYMSM6		Ig kappa chain precu	9.95e-77
4	806	85.6	132	2	KYMS32		Ig kappa chain precu	3.08e-75
5	805	85.5	131	5	PH1226		Ig kappa chain precu	4.01e-75
6	785	83.3	128	13	JU0073		aberrant kappa trans	7.84e-73
7	754	80.0	128	11	S52448		Ig kappa chain v reg	2.76e-69
8	741	78.7	111	2	KYMS84		Ig kappa chain v reg	8.41e-68
9	734	77.9	111	2	KYMS75		Ig kappa chain v reg	5.30e-67
10	725	77.0	111	2	KYMS60		Ig kappa chain v reg	5.63e-66
11	720	76.4	111	2	KYMS85		Ig kappa chain v reg	2.09e-65
12	713	75.7	112	12	S45715		antigen-Fab VL - pse	1.31e-64

Jul 8 08:18

US-08-137-117B-25.rpr

3

```
Db 61 qqkpgppklllylaasilesgvparfsgsgtdftlnihpveeedaatyqcqhreypl 120
Qy 61 QQKPGQTPKLLIYLASNLESQVPAFSGSGCTDFTLNHPVEEEDAATYYCQHSRENPY 120

Db 121 tfgggtkleik 131
Qy 121 TFGGGTKLEIK 131

RESULT 2
ENTRY      PN0446      #type fragment
TITLE      Ig kappa chain precursor V-II region - human (fragment)
ORGANISM   #formal name Homo sapiens #common name man
DATE       30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
          30-Apr-1995
ACCESSIONS PN0446
REFERENCE   PN0444
#authors   Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidie,
           U.H.
#journal   Gene (1997) 122:321-328
#title     A general method for chimerization of monoclonal antibodies
           by inverse polymerase chain reaction which conserves
           authentic N-terminal sequences.
#accession PN0446
#molecule_type mRNA
#residues  1-140 ##label KAL
#cross-references GB:L02345
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS    immunoglobulin
FEATURE     1-20      #domain signal sequence #status predicted #label SIG
           21-140    #product Ig light chain kappa-2 V region #status
           predicted #label MAT
SUMMARY     #length 140 #checksum 3597

Query Match      88.9%; Score 837; DB 5; Length 140;
Best Local Similarity 91.6%; Pred. No. 8.54e-79;
Matches 120; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

Db 1 metdtllllwllwvpgstgdivltqspaslavslgqratisykraskevstgysymhwn 60
Qy 1 MESDTLLWLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYMHY 60

Db 61 qqkpgppklllylvnlesgvparfsgsgtdftlnihpveeedaatyqcqhre--l 118
Qy 61 QQKPGQTPKLLIYLASNLESQVPAFSGSGCTDFTLNHPVEEEDAATYYCQHSRENPY 120

Db 119 tfgggtkleik 129
Qy 121 TFGGGTKLEIK 131

RESULT 3
ENTRY      KWMSM6      #type complete
TITLE      Ig kappa chain precursor V regions (M63, AB22, PC9245,
           PC4050) - mouse
ORGANISM   #formal name Mus musculus #common name house mouse
DATE       02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
          31-Dec-1993
ACCESSIONS B90412; B90374; B93822; C93204; D93204; A01935
REFERENCE   A90412
#authors   Burstein, Y.; Schechter, I.
#journal   Biochemistry (1978) 17:2392-2400
#title     Primary structures of N-terminal extra peptide segments
```

Jul 8 08:18

US-08-137-117B-25.rpr

4

```
linked to the variable and constant regions of
immunoglobulin light chain precursors: implications on the
organization and controlled expression of immunoglobulin
genes.
#cross-references MUID:78235887
#contents   M63
#accession  B90412
#molecule_type protein
#residues   1-35 ##label BUR
REFERENCE   A90374
#authors   McKean, D.; Potter, M.; Hood, L.
#journal   Biochemistry (1973) 12:760-771
#title     Mouse immunoglobulin chains. Pattern of sequence variation
           among kappa chains with limited sequence differences.
#cross-references MUID:73140225
#contents   M63
#accession  B90374
#molecule_type protein
#residues   21-46, 'Q', 48-53, 'B', 55-57, 'Z', 59-86, 'F', 88-131 ##label
           MCK
#note      this sequence has since been revised in reference A93822
REFERENCE   A93822
#authors   McKean, D.J.; Bell, M.; Potter, M.
#journal   Proc. Natl. Acad. Sci. U.S.A. (1978) 75:3913-3917
#title     Mechanisms of antibody diversity: multiple genes encode
           structurally related mouse kappa variable regions.
#cross-references MUID:79012520
#contents   M63; AB22
#accession  B93822
#molecule_type protein
#residues   1-53; 69-107 ##label MC2
#accession  C93822
#molecule_type protein
#residues   21-119, 'Y', 121-131 ##label MC3
REFERENCE   A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal   Nature (1978) 276:785-790
#title     Rearrangement of genetic information may produce
           immunoglobulin diversity.
#cross-references MUID:79073152
#contents   PC9245; PC4050
#accession  C93204
#molecule_type protein
#residues   21-119, 'Y', 121-131 ##label WEI
#accession  D93204
#molecule_type protein
#residues   21-119, 'L', 121-123, 'A', 125-129, 'L', 131 ##label WE2
COMMENT     The M63 precursor sequence is shown.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE     1-20      #domain signal sequence #status experimental #label SIG
SUMMARY     #length 131 #molecular-weight 14291 #checksum 5945

Query Match      86.9%; Score 819; DB 2; Length 131;
Best Local Similarity 84.7%; Pred. No. 9.95e-77;
Matches 111; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Db 1 metdtllllwllwvpgstgdivltqspaslavslgqratisykraskevstgysymhwy 60
Qy 1 MESDTLLWLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGYSYMHY 60

Db 61 qqkpgppklllylaasilesgvparfsgsgtdftlnihpveeedaatyqcqhnedpw 120
Qy 61 QQKPGQTPKLLIYLASNLESQVPAFSGSGCTDFTLNHPVEEEDAATYYCQHSRENPY 120
```

Jul 8 08:18

US-08-137-117B-25.rpt

5

Db 121 tfgggtkleik 131
|||||
Qy 121 TFGGGTKLEIK 131

RESULT 4
ENTRY KWMS2 #type complete
TITLE Ig kappa chain precursor V regions (MOPC 321, TEPC 124) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 31-May-1979 #sequence_revision 31-May-1979 #text_change 04-Nov-1994

ACCESSIONS A90412; A90373; A90374; A01933
REFERENCE A90412
#authors Burstein, Y.; Schechter, I.
#journal Biochemistry (1978) 17:2392-2400
#title Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.

#cross-references MUID:78235887
#contents MOPC 321
#accession A90412
##molecule_type protein
##residues 1-37 ##label BUR
##note this precursor was synthesized in a cell-free system directed by mRNA isolated from myeloma polyclones

REFERENCE A90373
#authors McKean, D.; Potter, M.; Hood, L.
#journal Biochemistry (1973) 12:749-759
#title Mouse immunoglobulin chains. Partial amino acid sequence of a kappa chain.

#cross-references MUID:73140224
#contents MOPC 321
#accession A90373
##molecule_type protein
##residues 21-132 ##label MCK
##note the partial sequence of the C region of this Bence Jones protein was also determined; it differs from that reported for mouse MOPC 21 only in the transposition of two nearby residues

REFERENCE A90374
#authors McKean, D.; Potter, M.; Hood, L.
#journal Biochemistry (1973) 12:760-771
#title Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.

#cross-references MUID:73140225
#contents TEPC 124
#accession A90374
##molecule_type protein
##residues 21-131 ##label MC2
##note the sequence is compatible with that of MOPC 321 except in having 47-Glx, 51-Trp, and 118-Ala

COMMENT The MOPC 321 sequence is shown.
COMMENT Residues 1-20 are the signal sequence.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

FEATURE 36-114
#domain immunoglobulin homology #label IMM

SUMMARY #length 132 #molecular-weight 14523 #checksum 370

Query Match 85.6%; Score 806; DB 2; Length 132;
Best Local Similarity 77.1%; Pred. No. 3.08e-75;

Jul 8 08:18

US-08-137-117B-25.rpt

6

Matches 101; Conservative 20; Mismatches 10; Indels 0; Gaps 0;

Db 1 metdtllwllwpgstgdivltqspaslvslgqratisckasqvntygnsfmzy 60
|||:|||||
Qy 1 MESDTLLWLLWPGSGTGDVLTQSPASLVSLGQRATISCRASKSVSTSGSYNMHWY 60

Db 61 zkpqzppklliyaaenlzagiparfsgsgtdftlnihpveedaatyycqhsrenpy 120
::|||:|||||
Qy 61 QQKPGQTPEKLLIYLAENLESQVPARFSGSGTDFTLNIHPVEEDAATYYCQHSRENPY 120

Db 121 tfgggtkleik 131
|||||
Qy 121 TFGGGTKLEIK 131

RESULT 5
ENTRY PH1226 #type fragment
TITLE Ig kappa chain precursor V region (M-T310) - human (fragment)
ORGANISM #formal name Homo sapiens #common name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 30-Apr-1995

ACCESSIONS PH1226
REFERENCE PH1224
#authors Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz, H.; Weiss, E.H.; Rieber, E.P.; Riethmueller, G.; Weidle, U.H.

#journal Gene (1992) 121:271-278
#title Combinatorial functions of two chimeric antibodies directed to human CD4 and one directed to the alpha-chain of the human interleukin-2 receptor.

#accession PH1226
##molecule_type mRNA
##residues 1-131 ##label WEI

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

KEYWORDS immunoglobulin

FEATURE 1-20 #domain signal sequence #status predicted #label SIGV
21-131 #product Ig light chain V region #status predicted #label MAT

SUMMARY #length 131 #checksum 4648

Query Match 85.5%; Score 805; DB 5; Length 131;
Best Local Similarity 85.5%; Pred. No. 4.01e-75;
Matches 112; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Db 1 metdtllwllwpgstgdivltqspaslvslgqratisckasqldydgdsymwy 60
|||:|||||
Qy 1 MESDTLLWLLWPGSGTGDVLTQSPASLVSLGQRATISCRASKSVSTSGSYNMHWY 60

Db 61 qkpqzppklliyaaenlzagiparfsgsgtdftlnihpveedaatyycqhsrenpy 120
|||||
Qy 61 QQKPGQTPEKLLIYLAENLESQVPARFSGSGTDFTLNIHPVEEDAATYYCQHSRENPY 120

Db 121 tfgggtkleik 131
|||||
Qy 121 TFGGGTKLEIK 131

RESULT 6
ENTRY JL0073 #type complete
TITLE aberrant kappa transcript - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 21-Nov-1993 #sequence_revision 21-Nov-1993 #text_change 21-Nov-1993

Jul 8 08:18

US-08-137-117B-25.rpr

7

```
ACCESSIONS      JL0073
REFERENCE        Carroll, W.L.; Mendel, E.; Levy, S.
#authors         Mol. Immunol. (1988) 25:991-995
#journal         Hybridoma fusion cell lines contain an aberrant kappa
#title           transcript.
#cross-references MUID:89112230
#accession       JL0073
#status          preliminary
#residues        1-128 ##label CAR
SUMMARY          #length 128 #molecular-weight 14060 #checksum 5564

Query Match      83.3%; Score 785; DB 13; Length 128;
Best Local Similarity 93.2%; Pred. No. 7,84e-73;
Matches 109; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 1 metdtdllwvllwpqstgdivltgspaslavslqqratisyrasksvstgysymhw 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLGVLGQRATISCRASKSVSTGYSYMHY 60

Db 61 qkpgqprlliylnlesgvparsfgsgsgtdftlnihpveedaatyqcqhre 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 QQKPGQTPKLLIYLASNLESVPARESGSGTGDTFTNIHPVEEDAATYYCQHSRE 117

RESULT 7
ENTRY        S52448      #type complete
TITLE        Ig kappa chain V region - mouse
ORGANISM     #formal_name Mus musculus #common_name house mouse
DATE         08-May-1995 #sequence_revision 21-Jul-1995 #text_change
              21-Jul-1995

ACCESSIONS   S52448
REFERENCE     S52445
#authors      Berdoz, J.; Kraehenbuhl, J.P.
#submission   submitted to the EMBL Data Library, November 1994
#description   Specific amplification by the polymerase chain reaction of
              rearranged genomic variable regions of immunoglobulin genes
              from mouse hybridoma cells.
#accession    S52448
#status       preliminary
#molecule_type DNA
#residues     1-128 ##label BER
#cross-references EMBL:X82689

GENETICS
#introns      14/1
SUMMARY       #length 128 #molecular-weight 14020 #checksum 5468

Query Match      80.0%; Score 754; DB 11; Length 128;
Best Local Similarity 90.7%; Pred. No. 2,76e-69;
Matches 107; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 metdtdllwvlllflpbgtdivltgspaslavslqqratisyrasksvstgysymhw 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 MESDTLLWVLLWV-PCSTGDIVLTQSPASLGVLGQRATISCRASKSVSTGYSYMHY 59

Db 61 nqkpgqprlliylnlesgvparsfgsgsgtdftlnihpveedaatyqcqhre 118
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 YQKPGQTPKLLIYLASNLESVPARESGSGTGDTFTNIHPVEEDAATYYCQHSRE 117

RESULT 8
ENTRY        KWS84      #type complete
TITLE        Ig kappa chain V region (PC6684) - mouse
ORGANISM     #formal_name Mus musculus #common_name house mouse
```

Jul 8 08:18

US-08-137-117B-25.rpr

8

```
DATE           01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
              11-Aug-1995
ACCESSIONS     A01938
REFERENCE       A93204
#authors        Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal        Nature (1978) 276:785-790
#title          Rearrangement of genetic information may produce
              immunoglobulin diversity.
#cross-references MUID:79073152
#accession      A01938
#molecule_type protein
#residues       1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE        16-94      #domain immunoglobulin homology #label IMM
              23-92      #disulfide bonds #status predicted
SUMMARY        #length 111 #molecular-weight 12039 #checksum 2467

Query Match      78.7%; Score 741; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 8,41e-68;
Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 divltgspaslavslqqratiscrasksvstgysymhwqkpgqpklliylnles 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLGVLGQRATISCRASKSVSTGYSYMHWYQKPGQTPKLLIYLASNLES 80

Db 61 gvparsfgsgtdftlnihpveedaatyqcqhrelptfgggtkleik 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GVPARESGSGTGDTFTNIHPVEEDAATYYCQHSRENPTFGGKTLEIK 131

RESULT 9
ENTRY        KWS75      #type complete
TITLE        Ig kappa chain V region (PC7175) - mouse
ORGANISM     #formal_name Mus musculus #common_name house mouse
DATE         30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
              30-Sep-1993

ACCESSIONS     B01938; A01938
REFERENCE       A93204
#authors        Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal        Nature (1978) 276:785-790
#title          Rearrangement of genetic information may produce
              immunoglobulin diversity.
#cross-references MUID:79073152
#accession      B01938
#molecule_type protein
#residues       1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       immunoglobulin
FEATURE        23-92      #disulfide bonds #status predicted
SUMMARY        #length 111 #molecular-weight 12010 #checksum 2086

Query Match      77.9%; Score 734; DB 2; Length 111;
Best Local Similarity 94.6%; Pred. No. 5,30e-67;
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 1 divltgspaslavslqqratiscrasksvstgysymhwqkpgqpklliylnles 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLGVLGQRATISCRASKSVSTGYSYMHWYQKPGQTPKLLIYLASNLES 80

Db 61 gvparsfgsgtdftlnihpveedaatyqcqhrelptfgggtkleik 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GVPARESGSGTGDTFTNIHPVEEDAATYYCQHSRENPTFGGKTLEIK 131
```

```
RESULT 10
ENTRY
TITLE      KvMS40      #type complete
ORGANISM   Ig kappa chain V region (PC7940) - mouse
DATE       #formal name Mus musculus #common name house mouse
           30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change
           30-Sep-1993
ACCESSIONS C01938; A01938
REFERENCE   A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal    Nature (1978) 276:785-790
#title      Rearrangement of genetic information may produce
            immunoglobulin diversity.
#cross-references MUID:79073152
#accession  C01938
#molecule_type protein
#residues   1-111 ##label WEI
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      immunoglobulin
FEATURE
23-92         #disulfide bonds #status predicted
SUMMARY       #length 111 #molecular-weight 12038 #checksum 2027

Query Match      77.0%; Score 725; DB 2; Length 111;
Best Local Similarity 93.7%; Pred. No. 5.63e-66;
Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 1 divltqspaslavlgqratiscrasksvafgysymhwycqgqppklliyasnlles 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 DIVLTQSPASLGVLGQRATISCRASKSVTSYGYSYMHYQQRPGQTPKLLIYASNLIES 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 gvparfsgsgtdftlnihpveeedavtycqhrelptlftgggtklelk 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 GVPARFSGSGTDFTLNIHPVEEEDAAITYYQHSRENPTYFGGGTKLEIK 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
ENTRY
TITLE      KvMS85      #type complete
ORGANISM   Ig kappa chain V regions (PC2485, PC4039) - mouse
DATE       #formal name Mus musculus #common name house mouse
           01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
           05-Apr-1995
ACCESSIONS A01939
REFERENCE   A93204
#authors   Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
#journal    Nature (1978) 276:785-790
#title      Rearrangement of genetic information may produce
            immunoglobulin diversity.
#cross-references MUID:79073152
#accession  A01939
#molecule_type protein
#residues   1-111 ##label WEI
#note       the PC4285 and PC4039 sequences are identical
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
23-92         #disulfide bonds #status predicted
SUMMARY       #length 111 #molecular-weight 11986 #checksum 2226

Query Match      76.4%; Score 720; DB 2; Length 111;
Best Local Similarity 91.9%; Pred. No. 2.09e-65;
Matches 102; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 1 divltqspaslavlgqratiscrasksvetegysymhwycqgqppklliyasnlles 60
```

```
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 DIVLTQSPASLGVLGQRATISCRASKSVTSYGYSYMHYQQRPGQTPKLLIYASNLIES 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 gvparfsgsgtdftlnihpveeedaaiycqhrelptlftgggtklelk 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 GVPARFSGSGTDFTLNIHPVEEEDAAITYYQHSRENPTYFGGGTKLEIK 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
ENTRY
TITLE      S45715      #type complete
ORGANISM   antigen-Fab VL - Pseudomonas aeruginosa
DATE       #formal name Pseudomonas aeruginosa
           10-Dec-1994 #sequence_revision 10-Dec-1994 #text_change
           10-Dec-1994
ACCESSIONS S45715
REFERENCE   S45714
#authors   Kim, H.H.; Kato, K.; Yamato, S.; Igarashi, T.; Matsunaga, C.;
            Ohtsuka, H.; Higuchi, A.; Nomura, N.; Noguchi, H.; Arata,
            Y.
#journal    FEBS Lett. (1994) 346:246-250
#title      Application of (13)C NMR spectroscopy to paratope mapping for
            larger antigen-Fab complexes.
#accession  S45715
#status     preliminary
#residues   1-112 ##label KIM
SUMMARY     #length 112 #molecular-weight 12168 #checksum 6129

Query Match      75.7%; Score 713; DB 12; Length 112;
Best Local Similarity 91.0%; Pred. No. 1.31e-64;
Matches 101; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 1 divltqspaslavlgqratiscrasksvstsgysymhwycqgqpprlliyasnlles 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 DIVLTQSPASLGVLGQRATISCRASKSVTSYGYSYMHYQQRPGQTPKLLIYASNLIES 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 gvparfsgsgtdftlnihpveeedaanyhcqhardlptlftgggtklelk 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 GVPARFSGSGTDFTLNIHPVEEEDAAITYYQHSRENPTYFGGGTKLEIK 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
ENTRY
TITLE      S06731      #type complete
ORGANISM   Ig kappa chain precursor - mouse
DATE       #formal name Mus musculus #common name house mouse
           20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
           12-Apr-1995
ACCESSIONS S06731
REFERENCE   S06731
#authors   Alaneh, A.; Weiss, S.
#journal    Eur. J. Immunol. (1989) 19:1961-1963
#title      Sequence and linkage of the V(kappa)21A and G germ-line gene
            segments in the mouse.
#cross-references MUID:90060210
#accession  S06731
#status     preliminary
#molecule_type DNA
#residues   1-120 ##label ALA
#cross-references EMBL:X16955
GENETICS
#introns    18/1
#superfamily immunoglobulin V region; immunoglobulin homology
CLASSIFICATION #length 120 #molecular-weight 13029 #checksum 5418
SUMMARY

Query Match      75.1%; Score 707; DB 5; Length 120;
```

2

```

RESULT      15
ENTRY
TITLE      Ig kappa chain V region (J528/32) - mouse
ORGANISM   Mus musculus #common name mouse
DATE       20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
           12-Apr-1995
ACCESSIONS S24288 #type complete
REFERENCE   S24288
            S24287 Moncharmont, B.
            submitted to the EMBL Data Library, September 1991
            Cloning and sequencing of the cDNA coding for the variable
            regions of the heavy and light chains of two monoclonal
            antibodies to the estrogen receptor.
            #accession S24288
            ##status preliminary
            #molecule_type mRNA
            ##residues 1-110 #label MON
            ##cross-references EMBL:X62703

```

Search completed: Mon Jul 8 08:28:44 1996
Job time : 21 secs.

FT	SIGNAL	1	20	IG KAPPA CHAIN V-III REGION (MOPC 63).
FT	CHAIN	21	131	FRAMEWORK 1.
FT	DOMAIN	21	43	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	44	58	FRAMEWORK 2.
FT	DOMAIN	59	73	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	74	80	FRAMEWORK 3.
FT	DOMAIN	81	112	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	113	121	FRAMEWORK 4.
FT	DOMAIN	122	131	BY SIMILARITY.
FT	DISULFID	43	112	
FT	NON TER	131	131	
SO	SEQUENCE	131 AA:	14291 MW:	90798 CN:

Query Match 86.9%; Score 819; DB 4; Length 131;
Best Local Similarity 84.7%; Pred. No. 1.27e-158;
Matches 111; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

```

Db      1 metdtllllwllwvpgstgnivltqspaslavlsgqratiscrasesvdsygnsfmhw 60
        ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      1 MSEDTLVLLWLLWVPGSTGDIVLTQSPASLVGLGQRATISCRASKSVSTGCGSYNMHW 60

```

```

61 qkqgqgppklllylasnlesgvparfsgsgrtftldpveaddaatyyoqgmndpw 120
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
61 QKQPGQTPLLIIYASNLESVPA RFSGSGCTFTLNHPVEEDATYYCOHSRENPY 120

```

Db 121 tfgggtkleik 131
|||
Qy 121 TFGGGTKLEIK 131

RESULT

ID	KV3F MOUSE	STANDARD;	PR7;	132 AA.
AC	P01658;			
DT	21-JUL-1986	(REL. 01, CREATED)		
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)		
DT	01-OCT-1993	(REL. 27, LAST ANNOTATION UPDATE)		
DE	IG KAPPA CHAIN PRECURSOR V-III REGION (MOPC 321).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHYRIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE OF 1-37.			
RM	7823587			
RA	BURSTEIN Y., SCHECHTER I.;			
RL	BIOCHEMISTRY 17:2392-2400 (1978).			

RD SEQUENCE OF 21-132

RM	13140224	1	100	1
13140224	1	100	1	1

RL BIOCHEMISTRY 12:749-759(1973).
 CC -:- THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN
 CC WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE
 CC MO κ C 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.

DR PIR; A01933; KVMS32

KW IMMUNOGLOBULIN V REGION: BENCE-JONES PROTEIN: SIGNAL:

FT	SIGNAL	1	20
FT	CHAIN	21	132
FT	DOMAIN	21	43

IG KAPPA CHAIN V-III REGION (MOPC 321).
FRAMEWORK 1.

FT	DOMAIN	44	58	COMPLEMENTARITY-DETERMINING 1.
----	--------	----	----	--------------------------------

FT	DOMAIN	59	73	FRAMEWORK 2.
----	--------	----	----	--------------

FT	DOMAIN	81	112	FRAMEWORK 3.
----	--------	----	-----	--------------

FT	DOMAIN	113	121
			COMPLEMENTARITY-DETERMINING 3.

FT	DOMAIN	122	131	FRAMEWORK 4.
FT	DISULFID	43	112	BY SIMILARITY.
FT	NON TER	132	132	
SQ	SEQUENCE	132 AA;	14523 MW;	114870 CN;

Query Match	85.6%;	Score 806;	DB 4;	Length 132;
Best Local Similarity	77.1%;	Pred. No. 1.36e-155;		
Matches 101;	Conservative	20;	Mismatches 10;	Indels 0; Gaps 0;

Db 1 metdtlllwwlllwyogstadi vltaspaslavslaaratiscrasksyntvgnsfmzwv 60

QV 1 MESDTLLWVLLWVPGSTGDIVLTOSPASLGVSLGORATISCRASKSVSTSGYSYMHWY 60

Db 61 zkkpazppkllivrasnlzsqiparfssqsrftltibpvzabdvatvfczzszbzbpw 120

61 QOKPGQTPKLLIYLASNLESGVPAFSCGSGTFTLNHPVEEDAAYYCQHSRENPY 120

1

Db 121 tfqsatkleik 131

䷊

Qy 121 TFGG^TKL^EIK 131

RESULT

ID	KV3R MOUSE	STANDARD;	PRT;	111 AA.
AC	P01670;			
DT	21-JUL-1986	(REL. 01, CREATED)		
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)		
DT	01-OCT-1993	(REL. 27, LAST ANNOTATION UPDATE)		
DE	IG KAPPA CHAIN V-III REGION	(PC 6684).		
OS	MUS MUSCULUS	(MOUSE).		
OC	EUKARYOTA;	CHORDATA;	VERTEBRATA;	TETRAPODA;
OC	EUKARYOTA;	METAZOA;	EUTHERIA;	RODENTIA.
				MAMMALIA;

RP
SEOT
[17]

RM	79073152	WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RA	NR	NATURE 276:785-790(1978).
RL	PIR: A01938; KVM84.	
RR	DR	HSP; P01679; IACV.
DR	KW	IMMUNOGLOBULIN V REGION.
FT	DOMAIN 1	23
FT	DOMAIN 24	38
FT	DOMAIN 39	53
FT	DOMAIN 54	60
FT	DOMAIN 61	92
FT	DOMAIN 93	101
FT	DOMAIN 102	111
FT	DISULFID 23	92
FT	NON TER 111	111
SO	SEQUENCE 111 AA:	12039 MW; 66692 CN;

Query Match 78.7%; Score 741; DB 4; Length 111;
Best Local Similarity 96.4%; Pred. No. 1.74e-140;
Matches 107; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 1 divltaspnslavslqaratiscrasksvstsqvsvmhvwaakpaaakllivlasnles 60

0v 21 DIVI.TOSPASLGVSLGORATISCRASKSVSTSGYSYMHYOOKPGOTPKLLIYASNIES 80

Figure 1

61 avparfsgasatdftlnihpveeedaatvvcchsrelprtfgaatkleik 111

81 GVPARFSGSGTDFTNIHHPVEEEDAATYYCOHSRENPHYFGGGTKLEIK 131

Jul 8 08:17

US-08-137-117B-25.rsp

5

```
RESULT 4
ID KV3S MOUSE STANDARD; PRT; 111 AA.
AC P01671;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7175).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79073152
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790 (1978).
DR PIR; B01938; KWS75.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12010 MW; 66974 CN;
```

Query Match 77.9%; Score 734; DB 4; Length 111;
Best Local Similarity 94.6%; Pred. No. 7.28e-139;
Matches 105; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Db 1 divltqspaslavslqqratiscrasksvstgysymhwqkpgqpkllylasnles 60
Qy 21 DIVLTQSPASLGVSIGQRATISCRASKSVSTGYSYMHYQKPGQTPKLLIYASNLES 80
Db 61 gvpafegsgsgtdftlnihpveedaatyycqhsreplptfgagtkleik 111
Qy 81 GVPARESGSGTDFTLNIHPVEEDAATYTCQHSRENPTFTGGGKLEIK 131
```

```
RESULT 5
ID KV3T MOUSE STANDARD; PRT; 111 AA.
AC P01672;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7940).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79073152
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790 (1978).
DR PIR; C01938; KWS40.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
```

Jul 8 08:17

US-08-137-117B-25.rsp

6

```
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12038 MW; 69104 CN;

Query Match 77.0%; Score 725; DB 4; Length 111;
Best Local Similarity 93.7%; Pred. No. 8.86e-137;
Matches 104; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Db 1 divltqspaslavslqqratiscrasksvstgysymhwqkpgqpkllylasnles 60
Qy 21 DIVLTQSPASLGVSIGQRATISCRASKSVSTGYSYMHYQKPGQTPKLLIYASNLES 80
Db 61 gvpafegsgsgtdftlnihpveedaatyycqhsreplptfgagtkleik 111
Qy 81 GVPARESGSGTDFTLNIHPVEEDAATYTCQHSRENPTFTGGGKLEIK 131
```

RESULT 6
ID KV3U MOUSE STANDARD; PRT; 111 AA.
AC P01673;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 2485 AND PC 4039).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79073152

```
RA WEIGERT M., GATWALTAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790 (1978).
CC -!- THE PC 4285 AND PC 4039 SEQUENCES ARE IDENTICAL.
DR PIR; A01939; KWS85.
DR HSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11986 MW; 66852 CN;
```

Query Match 76.4%; Score 720; DB 4; Length 111;
Best Local Similarity 91.9%; Pred. No. 1.27e-135;
Matches 102; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Db 1 divltqspaslavslqqratiscrasksvstgysymhwqkpgqpkllylasnles 60
Qy 21 DIVLTQSPASLGVSIGQRATISCRASKSVSTGYSYMHYQKPGQTPKLLIYASNLES 80
Db 61 gvpafegsgsgtdftlnihpveedaatyycqhsreplptfgagtkleik 111
Qy 81 GVPARESGSGTDFTLNIHPVEEDAATYTCQHSRENPTFTGGGKLEIK 131
```

RESULT 7

Jul 8 08:17

US-08-137-117B-25.rsp

7

```
ID KV3L MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (CHPC 101).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79012520
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
CC -!- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSSP; P01679; IGBB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; 65196 CN;
```

Query Match 72.6%; Score 684; DB 4; Length 111;
Best Local Similarity 86.5%; Pred. No. 2.67e-127;
Matches 96; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

```
Db 1 divltqspaslavslqgratiscasvdytgesymwvqgqgpklliyaaanles 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLVSLGRATISCRASKSVSTGYSYMHVYQKPGQTPKLLIYLAASLES 80
```

```
Db 61 giparfsgsgtdftlnihpveedaatyccqsgnedpytfgggtkleik 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GVPARESGSGTDFTLNIHPVEEDAATYCCQHSRENPTYFGGGTKLEIK 131
```

```
RESULT 8
ID KV3M MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (PC 7043).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 79073152
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
DR PIR; A01937; KVM543.
DR HSSP; P01679; IGBB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
```

Jul 8 08:17

US-08-137-117B-25.rsp

8

```
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 65350 CN;
```

Query Match 71.7%; Score 675; DB 4; Length 111;
Best Local Similarity 85.6%; Pred. No. 3.18e-125;
Matches 95; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

```
Db 1 divltqspaslavslqgratiscasvdydgsymwvqgqgpklliyaaanles 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLVSLGRATISCRASKSVSTGYSYMHVYQKPGQTPKLLIYLAASLES 80
```

```
Db 61 giparfsgsgtdftlnihpveedaatyccqsgnedpytfgggtkleik 111
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 81 GVPARESGSGTDFTLNIHPVEEDAATYCCQHSRENPTYFGGGTKLEIK 131
```

```
RESULT 9
ID KV3J MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-III REGION (ABPC 22 AND PC 9245).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP ABPC 22, SEQUENCE.
RM 79012520
RA MCKEAN D.J., BELL M., POTTER M.;
RL PROC. NATL. ACAD. SCI. U.S.A. 75:3913-3917(1978).
RN [2]
RP PC 9245, SEQUENCE.
RM 79073152
RA WEIGERT M., GATMAITAN L., LOH E., SCHILLING J., HOOD L.E.;
RL NATURE 276:785-790(1978).
CC -!- THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR PIR; A01935; KVM546.
DR HSSP; P01679; IACY.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; 64631 CN;
```

Query Match 71.3%; Score 672; DB 4; Length 111;
Best Local Similarity 83.8%; Pred. No. 1.56e-124;
Matches 93; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

```
Db 1 nivltqspaslavslqgratiscraesvdygnsfmhwvqgqgpklliyaaanles 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 21 DIVLTQSPASLVSLGRATISCRASKSVSTGYSYMHVYQKPGQTPKLLIYLAASLES 80
```

```
Db 61 gyparfsgsgtdftlnidpveadaatyccqsgnedpytfgggtkleik 111
```


Jul 8 08:17

US-08-137-117B-25.rsp

13

Db 61 giparfsgsgtdftlnihpveedaatyqhqs-edpwtfgsgtkleik 110

|:|||||||||||||||||||||:| |:|:|||||

Oy 81 CVPARFSGSGTDFTLNHPVEEDAATYQCQHSRENPYTFGGTKLEIK 131

Search completed: Mon Jul 8 08:28:04 1996

Job time : 12 secs.

W P S R E L L (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:29:02 1996; MasPar time 4.45 Seconds

Tabular output not generated. 243.853 Million cell updates/sec

Title: >US-08-137-117B-25

Description: (1-131) from US08137117B.pap

Perfect Score: 942

Sequence: 1 MESDPLLLVLLWLLVPGSTG.....CQHSRENPTFGGTYKLEIK 131

Scoring table: PAM 150
Gap 11

Searched: 70887 seqs, 8282111 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq22

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14

Statistics: Mean 30.229; Variance 161.993; scale 0.187

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description	Pred. No.
1	942	100.0	131	6	R28668	p12-k2.	Anti-idiotypic antibody	1.32e-63
2	851	90.3	130	14	R74967	Mouse MAb 3B9 light c	6.43e-54	1.96e-56
3	819	86.6	131	1	P90543	Amino acids sequence	1.11e-53	6.43e-54
4	816	86.6	131	1	P90543	Amino acids sequence	1.11e-53	6.43e-54
5	809	85.9	146	14	R74966	Anti-idiotypic antibody	3.93e-53	6.43e-54
6	805	85.5	131	6	R32123	Anti-CD4 antibody MT	8.10e-53	6.43e-54
7	797	84.6	131	1	R04132	Anti-Leu 3a light cha	3.44e-52	6.43e-54
8	786	83.4	131	6	R29008	p64-k4 protein produc	2.51e-51	6.43e-54
9	785	83.3	132	3	R10920	kappa light chain var	3.01e-51	6.43e-54
10	781	82.9	131	6	R30881	Antibody 4A2 light ch	6.20e-51	6.43e-54
11	768	81.5	131	1	R05089	Light chain variable	6.50e-50	6.43e-54
12	757	80.4	132	7	R37716	Mouse 4C10 anti-idiot	4.73e-49	6.43e-54

13	725	77.0	112	14	R80272	VL region from an ant	1.52e-46
14	716	76.0	110	11	R60564	Anti-carcinoembryonic	7.70e-46
15	706	74.9	112	2	R07456	N-terminal sequence o	4.67e-45
16	702	74.5	212	10	R52659	Porphyran antibody li	9.59e-45
17	701	74.4	124	3	R15442	Light chain variable	1.15e-44
18	696	73.9	110	14	R74956	Immunoglobulin light	2.82e-44
19	692	73.5	110	14	R74957	Immunoglobulin light	5.80e-44
20	687	72.9	112	14	R75431	Human thyroid stimula	1.43e-43
21	685	72.7	218	14	R75459	Mouse antibody F4-7 1	2.04e-43
22	685	72.7	218	14	R75457	Mouse antibody FB3-2	2.04e-43
23	684	72.6	111	11	R60528	Light chain variable	2.45e-43
24	683	72.5	125	3	R15440	Light chain variable	2.93e-43
25	671	71.2	111	10	R55123	Mouse anti-HIV mu5.5	2.53e-42
26	671	71.2	111	11	R60302	Anti HIV antibody lig	2.53e-42
27	663	70.4	111	1	P90541	Immunoglobulin L chai	1.07e-41
28	650	69.0	112	14	R79156	Human IgE receptor-bi	1.10e-40
29	649	68.9	112	14	R79158	Human IgE receptor-bi	1.32e-40
30	646	68.6	111	6	R33305	MaE11 light chain.	2.26e-40
31	644	68.4	111	13	R65172	Murine NM-01 variable	3.23e-40
32	642	68.2	111	9	R47494	Murine anti-CD18 Ab 6	4.63e-40
33	640	67.9	112	2	R10539	Chimeric MAB 9.2.27 1	6.63e-40
34	637	67.6	110	10	R60810	Light chain variable	1.14e-39
35	635	67.4	112	3	R13089	Murine 1B4 light chai	1.63e-39
36	632	67.1	121	9	R48615	Sequence of the monoc	3.78e-39
37	631	67.0	121	6	R33346	Sequence of the varia	3.33e-39
38	630	66.9	126	2	R06375	Anti-Tac light chain	3.99e-39
39	630	66.9	126	2	R24108	Humanised anti-Tac an	3.99e-39
40	629	66.8	106	6	R33309	MaE15 light chain.	4.77e-39
41	627	66.6	112	14	R74955	Immunoglobulin light	6.83e-39
42	627	66.6	118	14	R74965	Anti-idiotypic antibod	6.83e-39
43	627	66.6	120	9	R48618	Sequence of the monoc	6.83e-39
44	626	66.5	133	10	R59511	Sequence of the light	8.17e-39
45	617	65.5	120	9	R48620	Sequence of the light	4.10e-38

ALIGNMENTS

RESULT	1
ID	R28668 standard; Protein; 131 AA.
AC	R28668;
DT	30-MAR-1993 (first entry)
DE	p12-k2.
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; AUK12-20;
KW	plasmid; p12-k2; p12-h2.
OS	Synthetic.
EH	Key
FT	Peptide
FT	/note= "Signal peptide"
FT	Protein
FT	/note= "Mature peptide"
PN	W09219759-A.
PD	12-NOV-1992.
PR	24-APR-1992; J00544.
PR	25-APR-1991; JP-095476.
PR	19-FEB-1992; JP-032084.
PA	(CHUS) CHUGAI SEIYAKU KK.
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR	WPI; 92-398882/48.
DR	N-PSDB; Q30753.
PT	Reconstituted human antibody to human interleukin-6 receptor -
PT	has low antigenicity and contains mouse V-region complementarity
PT	determining regions
PS	Disclosure; Page 118; 207pp; Japanese.

CC The sequences given in R28668-69 were encoded by plasmid sequences
CC which were used in example to illustrate the production of a human
CC antibody which recognises human interleukin-6 receptor (IL-6R). The
CC antibody comprises light (L) chain and heavy (H) chain variable
CC regions which were derived from a mouse monoclonal antibody produced
CC from the hybridoma AUK12-20 which contained the plasmids p12-k2 and
CC p12-h2.
SQ Sequence 131 AA;

Query Match	100.0%;	Score 942;	DB 6;	Length 131;
Best Local Similarity	100.0%;	Pred. No. 1.32e-63;		
Matches 131;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				
Db	1	mesdillllwlllvpgetgdivltgspaslgvalgdratiscrasksvatsgysmhwy	60	
Qy	1	MESDILLWLLWLLVPGSTGDIVLTGSPASLGVSIGQRTATISCRASKSVTSQSYMHY	60	
Db	61	qkqgqgtpklliliasnlesgvparfsgsgsgtdftlnlhpvceedaatyyccshrenpy	120	
Qy	61	QKQPGGTPKLLIYLASNIESGVPARFSGSGSGTDTLNLHPVEEDAAATYYCQHSRENPY	120	
Db	121	tfgggtkkleik	131	
Qy	121	TFGGGTKLEIK	131	

RESULT 2

ID	R74967 standard; Protein; 130 AA.
AC	R74967;
DT	02-FEB-1996 (first entry)
DE	Anti-idiotyp antibody Idio20 clone 20XB1.
KW	Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
KW	complementarity determining region.
OS	Mus sp.
FT	Key
FT	Location/Qualifiers
FT	Peptide
FT	1..20
FT	/label= signal_peptide
PN	J07101999-A.
PD	18-APR-1995.
PF	06-OCT-1993; 272950.
PR	06-OCT-1993; JP-272950.
PA	(HAGI/) HAGIWARA Y.
PA	WPI; 95-182987/24.
DR	N-PSDB; Q90432.
PT	Novel anti-idiotyp antibody against an human anticancer monoclonal
PT	antibody - and DNA sequences encoding the antibody, useful in
PT	pharmacology, medicine and biochemical fields.
PS	Example 5; Page 20; 28pp; Japanese.
CC	R74960-R74969 are clones of the anti-idiotyp antibodies Idio3, Idio17,
CC	Idio20, Idio27 and Idio33 against a human anticancer monoconal antibody.
CC	These antibodies and DNA encoding them are useful in pharmacological,
CC	medical and biochemical fields of research.
SO	Sequence 130 AA;

	90.3%; Score 851; DB 14; Length 130; Best Local Similarity 90.1%; Pred.No.1.9e-56; Matches 118; Conservative 6; Mismatches 6; Indels 1; Gaps 1;
Db	1 metdtilllwllwpqstgdilvtgpaaslavslggrratigraskevstvsgysymbwn 60 :: 1 MESDTLLWLLWPQSTGDIVLTGPAASLVSLGGRRATIGRASKEVSTVSYYMHY 60
Db	61 qqrpgpprlliylvsnldsgvpafsegsgtgdflnhlpveeddaatyvcqli-eagay 119 :: :

Qy	61	QKQPGQTKLLIYLASNLSEGVAPRFGSGSGTDFTLNHPVEEDAATYYCQHSRENFY	120
Db	120	tfgggtkleik	130
Qy	121	TFGGGTkleIK	131

RESULT	3
ID	R70189 standard; Protein; 132 AA.
AC	R70189;
DT	20-SEP-1995 (first entry)
DE	Mouse Mab 3B9 light chain.
KW	Chimeric antibody; humanized antibody; antibody engineering;
KW	monoclonal antibody; MAb; interleukin-4; IL-4; allergy.
OS	Mus sp.
Key	Location/Qualifiers
FT	Peptide 1..20
FT	/label= Sig_peptide
FT	Region 44..58
FT	/label= CDR
FT	/note= "complementarity determining region"
FT	Region 74..80
FT	/label= CDR
FT	/note= "complementarity determining region"
FT	Region 113..121
FT	/label= CDR
FT	/note= "complementarity determining region"
PN	W09507301-A.
PD	16-MAR-1995.
PD	07-SEP-1994; U10308.
PR	07-SEP-1993; US-117366.
PR	14-OCT-1993; US-136783.
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PA	(SMIK) SMITHKLINE BEECHAM PLC.
PI	Gross MS, Holmes SD, Sylvester DR;
DR	WPI; 95-123387/16.
DR	N-PSDB; Q83490.
PT	Chimeric and humanised IL-4 monoclonal antibodies (mAbs), derived
PT	from high affinity mAbs - useful in treatment of IL-4-mediated
PT	and IgE-mediated allergic conditions
PS	Disclosure; Fig.1; 97pp; English.
CC	Spleen cells from mice immunized with human IL-4 were used to prepare
CC	hybridomas, which were screened for anti-IL-4 MAb secretion. Only
CC	clone 3B9 was positive. cDNA clones of the 3B9 light and heavy
CC	chains were cloned into pGEM7f+ and transformed into E. coli
CC	DH5-alpha. The clones were sequenced (Q83490-91), and used for
CC	antibody engineering.
SQ	Sequence 132 AA;
Query Match	86.9%; Score 819; DB 13; Length 132;
Best Local Similarity	87.0%; Pred. No. 6.43e-54;
Matches 114;	Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Db	1	metdtillwllwvpgstgdlvtgdpaslavslgratiekasksgvdydgsymnw	60
Qy	1	MESDTLLWLLWVPGSTGDLVTQSPASLGSVGLGORATISCRASKSVSTSGYSMMHY	60
Db	61	qdkpgqptklllvaanlesgiparfsgsgstgftlnlhpveeadaatyvcaqsnedpp	120
Qy	61	QXPGGTPTKLLIYLASNIESGVPARFSGSGSTGFTLNHPVEEADAATYVQHSRENPY	120
Db	121	tfgggtkleik	131
Qy	121	TFGGGTKEIK	131

RESULT	4	
ID	P90543 standard; protein; 131 AA.	
AC	P90543;	
DT:	20-OCT-1989 (first entry)	
DE	Amino acids sequence of a v chi region gene.	
KW	V cji region; immunoglobulin; L chain variable region; HIV.	
OS	Mus musculus	
PN	EP-327000-A.	
PD	09-AUG-1989.	
PF	30-JAN-1989; 101583.	
PR	30-JAN-1988; JP-20255.	
PR	08-JUL-1988; JP-171385.	
PT	The Chemo-Sero-Therapeutic Research Institute.	
PI	Maeda H, Eda Y, Kimachi K, Tokiyoshi S, Matsushita S, Hattori T,	
PI	Takatsuki K;	
DR	WPI; 89-229050/32.	
DR	N-PSDB; N90495.	
PT	Chimeric anti-human immune virus antibodies - contg. mouse variable	
PT	regions and human constant regions for diagnosis, treatment and	
PT	prevention of AIDS	
PS	Disclosure; Fig 8; 33pp; English.	
CC	The sequence is encoded by a v chi region gene (see N90495).	
CC	The sequence from Asp 21 encodes the L chain variable region.	
SC	Sequence 131 AA;	

	Query Match	86.4%;	Score 816;	DB 1;	Length 131;
	Best Local Similarity	85.5%;	Pred. No. 1,11e-53;		
	Matches	112;	Conservative	10;	Mismatches 9; Indels 0; Gaps 0;
Db	1 metdtilllwllwpqsgtdilvtqpaslaivlgqratisckasqvdyddgsymmyw	60			
	:: :: :: :: :: :: :: :: ::				
Qy	1 MESDTLLWLLVPCSTGDIVLTPSPASIGVSLGQRATISGRASKSVTSYCSYMHY	60			
Db	61 qkqpgppkliiaasnlesgiparfsgsgsrtdftlnihpveeedaatyyccgsndpf	120			
	:: :: :: :: :: :: :: ::				
Qy	61 QXPGGTPLKLIYILASNLESGBPARESGSGGTDFTLNIHPVEEDAAATYYCQRSRENPY	120			
Db	121 tfgsgtkleik	131			
	:: :: :: :: :: :: :: ::				
Qy	121 TFGGGTKLEIK	131			

RESULT	5	
ID	R74966 standard; Protein; 146 AA.	
AC	R74966;	
DT	02-FEB-1996 (first entry)	
DE	Anti-idiotypic antibody Id1017 clone 17Kb1.	
KW	Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;	
KW	complementarity determining region.	
OS	Mus sp.	
FO		Location/Qualifiers
FT	Key	1..13
FT	Peptide	
FT	/label= signal_peptide	
PN	J07101999-A.	
PD	18-APR-1995.	
PF	06-OCT-1993; 272950.	
PR	06-OCT-1993; JP-272950.	
PA	(HAGI7) HAGIWARA Y.	
DR	WPI; 95-182987/24.	
DR	N-PSDB; Q90431.	
PT	Novel anti-idiotypic antibody against an human anticancer monoclonal	
FT	antibody - and DNA sequences encoding the antibody, useful in	

PT Pharmacology, medicine and biochemical fields.
PS Example 5; Page 19, 28pp; Japanese.
PC R74960-R74969 are clones of the anti-idiotypic antibodies Id103, Id107, Id1020, Id1021 and Id1033 against a human anticancer monoclonal antibody.
CC These antibodies and DNA encoding them are useful in pharmacological, medical and biochemical fields of research.
SQ Sequence 146 AA;

Query Match 85.9%; Score 809; DB 14; Length 146;
Best Local Similarity 91.1%; Pred. No. 3.93e-53;
Matches 113; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Db 1 lwvlllwpvgstgdivltspasplavslgqrasisyrasksvstsgysymhwnqtkpqp 60
|||||

QY 8 LWVLLWVPGSTGDIVLTQSPASLGVLGQRATISCRASKSVSTSGYSYMHVYQKPGQT 67

```

D5 61 prillyvsn.lesgvpar.rsgsgsgtdtlnhpveeedaatycqnii-daytfgggtk 12
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qw 68 pKIIIVIA SNIESGVPARESCSCSCTDETINHPVEEEDAATVYCOHSBENPYTEGGCTK 12

```

Db 120 leik 123

Qy 128 LEIK 131

RESULT 6

ID R32123 standard; Protein; 131 AA.

AC R32123;

BT 02-JUN-1993 (first entry)
 DF Anti-COM contributed: MM 3 10

DE Anti-CD4 antibody MI 3.10 Tissue transplantation; graft: 1. ch

KW T-helper cell inhibition; transplant rejection; MAb;

KW interleukin-2 receptor.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT	Peptide	1..20
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20

FT	/label= signal	21	120
FT	Region		

```
FT region
FT /label= Variable
FT z1...120
```

FT	Region	121..131
FT	Region	121..131

FT /label= J1

PN DE4143214-A.

PD 28-JAN-1993.
DE 30 DEC 1001. 143314

PR 30=DEC=1991; 143214.
PR 25=JUL=1991: DE=124759.

PR 30-DEC-1991: DE-143214;

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

PI Kaluza B, Riethmueller G, Scheuer W, Weidle U;

DR WPI; 93-037582/

DR N-PSDB; Q36609.

PI synergistic antibody compsn. for use as immunosuppressant -
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R

PT alpha- or anti-IL2R beta antibodies

PS Claim 5; Page 11; 18pp; German.

CC This sequence is the Light chain

CC anti-CD4 monoclonal antibody for

CC composition. MAb MT 3.10 is deposited as clone 3.101/sB10 (ECACC

CC 50050/02): The anti-CD4 antibody is used which at least one anti-IL2R antibody or beta antibody. Individually the antibodies are strongly

CC alpha 2 beta antibody: individually the antibodies are secondary
CC inhibiting and when used together their immunosuppressive properties

CC are improved; they synergistically inhibit T-helper cell

CC proliferation to effectively inhibit transplant rejection at low

CC doses without significantly reducing the general immune response.

CC See also Q36608-Q36616.
CO commence 121 22.

sequence TCT AAA/

Jul 8 08:19

US-08-137-117B-25.rag

7

```
Query Match      85.5%; Score 805; DB 6; Length 131;
Best Local Similarity 85.5%; Pred. No. 8.10e-53;
Matches 112; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Db      1 metdtkllwllwvpgstgdivltqspaelpmslqgratiscaksgldydgdsymwy 60
        ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Qy      1 MESDTLLWLLWVPGSTGDIVLTQSPASLVGSLGQRATISCRASKSVSTGYSYMHY 60

Db      61 qkqpgppklliyaanlesgiparfsgsgtdftlnihpveedaatyccgsedpp 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      61 QQKPGQTPKLLIYLASNLESVPARFSGSGTDTLTNIHPVEEDAATYYCQHSRENPY 120

Db      121 tfaggtkleik 131
        ||||| |||||
Qy      121 TFGGGTKLEIK 131

RESULT 7
ID      R04132 standard; protein; 131 AA.
AC      R04132;
DE      06-SEP-1990 (first entry)
DT      Anti-Leu 3a light chain variable region gene product, 206 Vx.
KW      HIV; AIDS; anti-Leu3A; vaccine; ds.
OS      Mus musculus.
PN      EP-365209-A.
PD      25-APR-1990.
PF      11-OCT-1989; 010415.
PR      17-OCT-1988; US-260558.
PA      (BECT) Becton Dickinson Co.
PI      Hinton R, OI VT;
DR      N-PSDB; Q04039.
PT      New chimeric variants of murine antibody anti-leucine -
PS      contg. human antibody regions, and DNA encoding sequences.
CC      Claim 1; Fig 2; 12pp; English.
CC      Variants of murine monoclonal anti-CD4 antibody, anti-leu3A can be
CC      used to form chimeric mouse-variable, human-constant region Abs
CC      suggested as being useful as a vaccine to HIV.
SQ      Sequence 131 AA;

Query Match      84.6%; Score 797; DB 1; Length 131;
Best Local Similarity 84.0%; Pred. No. 3.44e-52;
Matches 110; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

Db      1 metdtkllwllwvpgstgdivltqspaelpmslqgratiscaksgldydgdsymwy 60
        ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Qy      1 MESDTLLWLLWVPGSTGDIVLTQSPASLVGSLGQRATISCRASKSVSTGYSYMHY 60

Db      61 qkqpgppklliyaanlesgiparfsgsgtdftlnihpveedaatyccgsedpp 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      61 QQKPGQTPKLLIYLASNLESVPARFSGSGTDTLTNIHPVEEDAATYYCQHSRENPY 120

Db      121 tfaggtkleik 131
        ||:||||:|
Qy      121 TFGGGTKLEIK 131

RESULT 8
ID      R29008 standard; Protein; 131 AA.
AC      R29008;
DT      30-MAR-1993 (first entry)
DE      p64-k4 protein product.
KW      Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
```

Jul 8 08:19

US-08-137-117B-25.rag

8

```
KW      heavy chain; variable region; mouse; monoclonal; hybridoma; AUK64-7;
KW      plasmid; p64-k4; p64-h2.
OS      Synthetic.
FH      Key      Location/Qualifiers
FT      Peptide      1..20
FT      /note= "signal peptide"
FT      Protein      21..131
FT      /note= "Mature peptide"
PN      W09219759-A.
PD      12-NOV-1992.
PF      24-APR-1992; J00544.
PR      25-APR-1991; JP-095476.
PR      19-FEB-1992; JP-032084.
PA      (CHUS ) CHUGAI SEIYAKU KK.
PI      Bendig MW, Jones ST, Saldanha JW, Sato K, Teuchiya M;
DR      WPI; 92-398882/48.
DR      N-PSDB; Q30757.
PT      Reconstituted human antibody to human interleukin-6 receptor -
PT      has low antigenicity and contains mouse V-region complementarity
PT      determining regions
PS      Disclosure; Page 124-125; 207pp; Japanese.
CC      The sequences given in R29008-09 were encoded by plasmids which were
CC      used in example to illustrate the production of a human antibody which
CC      recognises human interleukin-6 receptor (IL-6R). The antibody
CC      comprises light (L) chain and heavy (H) chain variable regions which
CC      were derived from a mouse monoclonal antibody produced from the
CC      hybridoma AUK64-7 which contained the plasmids p64-k4 and p64-h2.
SQ      Sequence 131 AA;

Query Match      83.4%; Score 786; DB 6; Length 131;
Best Local Similarity 82.4%; Pred. No. 2.51e-51;
Matches 108; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Db      1 mesdtkllwllwvpgstgdivltqspaelpmslqgratiscrasksvstgysymhy 60
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1 MESDTLLWLLWVPGSTGDIVLTQSPASLVGSLGQRATISCRASKSVSTGYSYMHY 60

Db      61 qkqpgppklliyaanlesgiparfsgsgtdftlnihpveedaatyccgsedpp 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      61 QQKPGQTPKLLIYLASNLESVPARFSGSGTDTLTNIHPVEEDAATYYCQHSRENPY 120

Db      121 tfaggtkleik 131
        ||:||||:|
Qy      121 TFGGGTKLEIK 131

RESULT 9
ID      RI0920 standard; Protein; 132 AA.
AC      RI0920;
DT      08-MAY-1991 (first entry)
DE      kappa light chain variable region of T84.66 monoclonal antibody.
KW      MAb T84.66; kappa light chain; carcinoembryonic antigen; CEA;
KW      human adenocarcinoma; mouse-human chimaeric antibody.
OS      Mus musculus.
FH      Key      Location/Qualifiers
FT      Peptide      21..38
FT      /label= tryptic peptide
FT      /note= "sequenced as peptide fragment"
FT      Region      44..57
FT      /label= complementarity determining region
FT      Region      70..80
FT      /label= complementarity determining region
FT      Region      110..121
FT      /label= complementarity determining region
```

PN W09101990-A.
PD 21-FEB-1991.
PF 19-JUL-1990; U004049.
PR 26-JUL-1989; US-385102.
PI (CITY) CITY OF HOPE.
PA Shively JE, Riggs AD, Neumaier M;
DR WPI; 91-073486/10.
DR N-PSDB; Q10834.
PT Novel anti-CEA antibody - comparable to ATCC Accession No. BH
PT 8747, produced by recombinant DNA, used in diagnosis of tumours
PS Claim 4; Page 18; 24pp; English.
CC The light chain variable region of murine MAB 84.66 was cloned and
CC sequenced. It was used to produce mouse V-human C antibodies with high
CC affinity for CEA. Chimeric murine-human anti-CEA Abs are used to
CC diagnose human colon adenocarcinomas.
CC See also Q11098 and Q10835-Q10848.
SQ Sequence 132 AA;

Query Match 83.3%; Score 785; DB 3; Length 132;
Best Local Similarity 79.4%; Pred. No. 3.01e-51;
Matches 104; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

Db 1 metdtllllwllwpgstgdivltqspaslavslqgratmscrageavdvgvflhw 60
||:|||||
Qy 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGSYMHWY 60
|||||
Db 61 qkqgpgpklliyasnesgiprvfsgtgrtdtliidpveaddvatycqgtneqpy 120
|||||
Qy 61 QKQPGQTPKLLIYLASNIESGVPARFSGSGGTDTLNIHPVEEDAATYYCQHSRENPY 120
|||||

Db 121 tfgggtkleik 131
|||||

Qy 121 TFGGKTLEIK 131

RESULT 10

ID R30881 standard; Protein; 131 AA.
AC R30881;
DT 10-MAY-1993 (first entry)
DE Antibody 4A2 light chain constant region.
KW Fd'; fragment; human; 4A2; constant region; Fab'; F(ab')2; antibody;
KW light chain; primer.
OS Mus musculus.
PN W09222324-A.
PD 23-DEC-1992.
PF 15-JUN-1992; U004976.
PR 14-JUN-1991; US-714175.
PA (XOMA) XOMA CORP.
PI Better MD, Carroll S, Horwitz AH;
DR WPI; 93-017909/02.
DR P-PSDB; Q34575.
PT Polynucleotide sequences encoding Fab' and F(ab')2 fragments -
PT used to produce, e.g. antibody-ricin A chain immuno:toxin(s)
PS Disclosure; Fig 10; 92pp; English.
CC This sequence represents the light chain constant domain (CL) from
CC mouse antibody 4A2. This sequence was used in conjunction
CC with the Fd' sequences given in Q34567-72 to produce chimeric Fd'
CC vectors.
SQ Sequence 131 AA;

Query Match 82.9%; Score 781; DB 6; Length 131;
Best Local Similarity 84.0%; Pred. No. 6.20e-51;
Matches 110; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Db 1 nesdtllllwllwpgstgdivltqspaslavslqgratmscrageavdvgvflhw 60
|||||
Qy 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGSYMHWY 60
|||||
Db 61 qkqgpgpklliyasnesgiprvfsgtgrtdfslnihpveediamyfcqgkrkvpw 120
|||||
Qy 61 QKQPGQTPKLLIYLASNIESGVPARFSGSGGTDTLNIHPVEEDAATYYCQHSRENPY 120
|||||
Db 121 tfgggtkleik 131
|||||

Qy 121 TFGGKTLEIK 131

RESULT 11

ID R05089 standard; protein; 131 AA.
AC R05089;
DT 04-OCT-1990 (first entry)
DE Light chain variable domain of human chorion gonadotropin-binding peptd.
KW Human chorionic gonadotropin; antibodies; choriocarcinoma; abortion;
KW tumour detection; complementary determining regions;
KW pregnancy prevention; light chain.
OS Mus musculus.
FH Key Location/Qualifiers
FT Binding-site 44..58
FT /label=CDR 74..80
FT Binding-site 113..120
FT /label=CDR
FT /label=CDR
PN EP-370581-A.
PD 30-MAY-1990.
PF 21-NOV-1989; 202951.
PR 25-NOV-1988; NL-002902.
PA (ALKU) AKZO NV.
PI van Wezenbeek PM;
DR WPI; 90-165307/22.
DR N-PSDB; Q04694.
PT Polypeptide(s) which specifically bind human chorionic gonadotropin -
PT contg. antigen-binding domains comprising complementary
PT determining domains.
PS Disclosure; P; English.
CC Together with the heavy chain variable domain (R05090) the sequence forms
CC a hCG-binding antibody fragment (FhCG). For the production of Abs
CC the variable region was fused to a constant region of human origin.
CC The product can be used to prevent pregnancy or for combatting
CC choriocarcinomas or other hCG-producing tumours.
CC They also have diagnostic applications as immune reagents for in vivo
CC diagnosis, eg for localisation of tumours and for in vitro diagnosis for
CC detection of hCG in body fluids.
SQ Sequence 131 AA;

Query Match 81.5%; Score 768; DB 1; Length 131;
Best Local Similarity 79.4%; Pred. No. 6.50e-50;
Matches 104; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

Db 1 mekdtllllwllwpgstgdivltqspaslavslqgratmscrageavdvgvflhw 60
|||||
Qy 1 MESDTLLWVLLWVPGSTGDIVLTQSPASLGVSIGQRATISCRASKSVSTSGSYMHWY 60
|||||

Db 61 qkqgpgpklliyasnesgiprvfsgtgrtdfslnihpveedtamycqgkvevpp 120
|||||

Qy 61 QKQPGQTPKLLIYLASNIESGVPARFSGSGGTDTLNIHPVEEDAATYYCQHSRENPY 120
|||||

Db 121 tfgggtkleik 131

Jul 8 08:19

US-08-137-117B-25.rag

11

```

QY 121 TFGGKLEIK 131
|||||
RESULT 12
ID R37116 standard; Protein; 132 AA.
AC R37116;
DT 30-SEP-1993 (first entry)
DE Mouse 4C10 anti-idiotypic Ab light chain V region.
KW MAIA; monoclonal antibody; hybridoma; organ transplant rejection;
KW immuno-modulator; cancer; treatment; diagnosis; melanoma;
KW anti-cancer immunity; enhancement; suppression.
OS Mus musculus.
FH Key Location/Qualifiers
FT Misc_difference 31
FT /note= "Thr -> Ser, from PCR substituted gene"
PN W09310221-A.
PD 27-MAY-1993.
PF 12-NOV-1992; U10166.
PR 13-NOV-1991; US-791934.
PA (REGC ) UNIV CALIFORNIA.
PI Hastings A, Irie RF, Morrison SL.
DR WPI; 93-182538/22.
PT Chimeric murine-human anti-idiotypic monoclonal antibodies -
PT useful as immuno-modulators for treating and diagnosing cancers,
PT and for suppressing organ transplant rejection and auto-immune
PT diseases
PS Disclosure; Page 30-31; 46pp; English.
CC The sequence is that of the 4C10 anti-idiotypic Ab light chain V region
CC which was used in the construction of a murine/human monoclonal
CC anti-idiotypic antibody (MAIA). The MAIA elicits an anti-ganglioside
CC response and produces antibodies which induce cytotoxic destruction
CC of cancer cells bearing the gangliosides. It can be used for treating
CC cancers partic. melanomas. It can also be used as an immunomodulator to
CC enhance anti-cancer immunity, suppress organ transplant rejection and
CC suppress auto-immune disease. The MAIA can also be used in the diagnosis
CC of cancers.
SQ Sequence 132 AA;
Query Match 80.4%; Score 757; DB 7; Length 132;
Best Local Similarity 79.5%; Pred. No. 4.73e-49;
Matches 105; Conservative 11; Mismatches 15; Indels 1; Gaps 1;
Db 1 metdltllwllwvpgtgdvltqspaelavlgqrattmcraseavdsvnsmfhw 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 1 MESDTLLWLLWVPGTGDVLTQSPASVIGVSGRATISCRASKSVSTGYSYMHY 60
Db 61 qkpgqppklllyrasklegiparfsgseerdtltinpveaddvatvycqnedpt 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 61 QKPGQTPKLLIYASNLSEGVPRFSGSGGDTFTLNHPVEEDAATYYCQHSRNP- 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 121 wtfgggwklek 132
|||||
QY 120 YTFGGGKLEIK 131
RESULT 13
ID R80272 standard; Protein; 112 AA.
AC R80272;
DT 27-FEB-1996 (first entry)
DE V1 region from an antibody against cancer-specific mucin.
KW Antibody; heavy chain; light chain; variable region; cancer; mucin;
KW hybridoma cell; murine; mouse; pancreatic cancer cell; expression vector;
KW Fv; human; constant domain; chimera; anaphylaxis.

```

Jul 8 08:19

US-08-137-117B-25.rag

12

```

OS Synthetic.
FH Key Location/Qualifiers
FT Domain 24..38
FT /label= CDR1
FT Domain 54..60
FT /label= CDR2
FT Misc_difference 64
FT /note= "encoded by GAG"
FT Domain 93..101
FT /label= CDR3
PN FR2714915-A1.
PD 13-JUL-1995.
PF 13-JAN-1994; JP-002131.
PR (TOX) ) TOSOH CORP.
PA Chung Y, Iba Y, Kaneko T, Sowa M, Yasukawa K;
PI WPI; 95-247908/33.
DR N-PSDB; Q98534.
CC New variable domains of antibody recognising cancer specific mucin
CC - and related DNA and expression vectors, producing chimeric
CC mouse-human antibody for diagnosis and treatment of cancer
CC Claim 6; Page 16-17; 25pp; French.
CC The amino acid sequence of the variable region from the light chain of an
CC antibody against cancer-specific mucin. The coding sequence was isolated
CC from M2 hybridoma cells expressing a murine antibody reactive with
CC pancreatic cancer cells. The DNA encoding the antibody variable regions
CC from the heavy (Q98533) and light chains were isolated and inserted into
CC vectors. These vectors express the domains as an Fv antibody. Vectors
CC which additionally contain genes encoding the human constant domains
CC express a chimeric mouse-human antibody. The antibodies are useful in
CC the detection and treatment of cancer. The chimeras should be less likely
CC to cause anaphylaxis than the original murine antibody.
SQ Sequence 112 AA;
Query Match 77.0%; Score 725; DB 14; Length 112;
Best Local Similarity 91.9%; Pred. No. 1.52e-46;
Matches 102; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Db 1 divltqspaslavlgqrattmcrasksvttdsfaymhwgkpgqppklllylasnles 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 21 DIVLTQSPASVIGVSGRATISCRASKSVSTGYSYMHYQKPGQTPKLLIYASNLSE 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 gvpdrfsgsgtdftlnhpveeedaatvycqhserefpwtfggktleik 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 81 GVPARFSGSGGDTFTLNHPVEEDAATYYCQHSRNPYTFGGGKLEIK 131
RESULT 14
ID R60564 standard; Protein; 110 AA.
AC R60564;
DT 25-APR-1995 (first entry)
DE Anti-carcinoembryonic antigen chimeric light chain Ab.
KW Anti-carcinoembryonic antigen chimeric antibodies; CEAS;
KW chimeric human-murine; breast or colorectal carcinoma;
KW light chain.
OS Chimeric Mus muscaris.
PN W09419466-A.
PD 01-SEP-1994.
PF 16-FEB-1994; U01709.
PR 16-FEB-1993; US-017570.
PA (DOWC ) DOW CHEM CO.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Goullie BB, Kaplan DA, Mezes PS, Rixon MM, Schlom J;

```

Search completed: Mon Jul 8 08:29:28 1996
Job time : 26 secs.

WAP5RL4 (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Mon Jul 8 08:38:26 1996; MacPar time 279.00 Seconds
Tabular output not generated. 1027.715 Million cell updates/sec

Title: >US-08-137-117B-26
Description: (1-405) from US08137117B.seq
Perfect Score: 405
N.A. Sequence: 1 ATGGGATGGAGCGGATCTT.....CTCTGTCACATGCTCTGCA 405
Comp: TACCTTACTTCGCCCTAGAA.....GAGACGATGACAGACGT

claim 135

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 264399 seqs, 353985056 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new11
1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN
9:PRI1 10:PRI2 11:PRI3 12:PRO1 13:PRO2 14:ROD 15:SYN
16:UNC 17:VRT 18:VIR

Database: genbank91
19:BCT1 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7
26:INV1 27:INV2 28:INV3 29:INV4 30:INV5 31:MAM1 32:MAM2
33:PAT1 34:PAT2 35:PAT3 36:PHG 37:PLN1 38:PLN2 39:PLN3
40:PLN4 41:PLN5 42:PLN6 43:PLN7 44:PRI1 45:PRI2 46:PRI3
47:PRI4 48:PRI5 49:PRI6 50:PRI7 51:PRI8 52:PRI9 53:ROD1
54:ROD2 55:ROD3 56:ROD4 57:ROD5 58:ROD6 59:ROD7 60:STR
61:SYN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5
68:VRL6 69:VRT1 70:VRT2 71:VRT3

Database: genbank-new11
72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN
79:PRI1 80:PRI2 81:PRI3 82:ROD 83:STR 84:SYN 85:UNA
86:VRL 87:VRT
u-emb144_91
88:part1

Statistics: Mean 10.395; Variance 4.346; scale 2.392

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	312	77.0	462	56	MUSIGKCLS	Mouse IgMk rearranged 4.07e-274
2	307	75.8	405	56	MUSIGHM195	Mus musculus Ig heavy 4.32e-269
3	296	73.1	421	59	S51851	M104E myeloma immunog 4.83e-258
4	292	72.1	440	55	MUSHA5	Mouse active H-chain 4.99e-254
5	286	70.6	291	56	MUSIGHZ2H	Mouse Ig germline hea 5.20e-248
6	285	70.4	440	55	MUSHA3	Mouse active H-chain 5.23e-247
7	284	70.1	440	55	MUSHA6	Mouse Ig active H-chain 5.25e-246
8	283	69.9	408	56	MUSIGHFV	Mouse Ig active alpha 5.28e-245
9	282	69.6	348	53	MDICMVAU	M.domesticus IgM vari 5.31e-244
10	281	69.4	440	55	MUSHA4	Mouse active H-chain 5.33e-243
11	279	68.9	450	33	A07953	Artificial sequence f 5.37e-241
12	278	68.6	348	53	MDICMVBG	M.domesticus IgM vari 5.39e-240
13	278	68.6	2908	56	MUSIGHZ2F	Mouse Ig rearranged h 5.39e-240
14	273	67.4	412	56	MUSIGHFX	Mouse Ig family J558 5.47e-235
15	273	67.4	414	35	I05341	Sequence 3 from paten 5.47e-235
16	273	67.4	414	56	MUSIGCAJB	Mouse Ig gamma active 5.47e-235
17	272	67.2	348	55	MUSANTDNAM	Mouse anti-DNA antibo 5.48e-234
18	272	67.2	547	56	MUSIGHAPA	Mouse Ig rearranged H 5.48e-234
19	270	66.7	429	56	MUSIGGBV	Mus musculus anti-HIV 5.49e-232
20	270	66.7	484	56	MUSIGH4C11	Mouse IgH chain mRNA, 5.49e-232
21	270	66.7	490	56	MUSIG4C11A	Mouse anti-idotype im 5.49e-232
22	267	65.9	451	55	MUSANTVDJ	Mouse anti-DNA autoan 5.50e-229
23	267	65.9	588	34	A23165	Artificial construct 5.50e-229
24	267	65.9	588	56	MUSIGGVAZ	Mus musculus IgG chai 5.50e-229
25	266	65.7	411	56	MUSIGHFY	Mouse Ig family J558 5.49e-228
26	265	65.4	342	56	MUSIGHADY	Mouse Ig heavy-chain 5.49e-227
27	265	65.4	352	53	MMIGIKH3	Mouse mRNA fragment f 5.49e-227
28	265	65.4	414	56	MUSIHCB	Mus musculus immunogl 5.49e-227
29	265	65.4	462	56	MUSIGHXZ	Mouse Ig rearranged g 5.49e-227
30	264	65.2	352	53	MMIGIKH4	Mouse mRNA fragment f 5.49e-226
31	263	64.9	474	54	MMAB1G3	M.musculus Mab 1G3 mR 5.48e-225
32	262	64.7	601	56	MUSIGHVA	Mouse Ig unrearranged 5.47e-224
33	261	64.4	351	59	S54755	IgG3 VH-anti-DNA IgG3 5.46e-223
34	261	64.4	509	56	MUSIGHAAG	Mouse Ig rearranged g 5.46e-223
35	260	64.2	454	53	MMIGHVDJ	M.musculus mRNA for i 5.45e-222
36	259	64.0	354	53	MMBV1619H	M.musculus heavy chai 5.43e-221
37	259	64.0	653	54	MMIGHV9	Mouse germline immuno 5.43e-221
38	259	64.0	767	56	MUSIGHVK2	Mouse Ig germline H-c 5.43e-221
39	258	63.7	352	54	MMIGHVR1	Mouse mRNA fragment f 5.42e-220
40	258	63.7	383	55	MMU28805	Mus musculus MoAb Mc3 5.42e-220
41	258	63.7	401	56	MUSIGKXE	Mouse Ig active gamma 5.42e-220
42	258	63.7	508	56	MUSIGF63A	Mouse anti-idotype im 5.42e-220
43	258	63.7	821	55	MMU26990	Mus musculus, isolate 5.42e-220
44	258	63.7	871	14	MM26990	Mus musculus, isolate 5.42e-220
45	258	63.7	1518	56	MUSIGAZA	Mouse Ig rearranged g 5.42e-220

ALIGNMENTS

RESULT 1
LOCUS MUSIGKCLS 462 bp mRNA ROD 15-MAR-1989
DEFINITION Mouse IgMk rearranged heavy-chain mRNA variable region (V-D-J)
anti-DNA_autoantibody.
ACCESSION M20831
KEYWORDS V-region; autoantibody; immunoglobulin heavy chain.
SOURCE Mouse (strain (NZBXW)F-1) spleen hybridoma cell line BXW-DNA16,
cDNA to mRNA.
ORGANISM Mus musculus

Jul 8 08:32

US-08-137-117B-26.gp

3

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE
AUTHORS Kofler, R., Strohal, R., Balderas, R.S., Johnson, M.E., Noonan, D.J.,
Duchosal, M.A., Dixon, F.J. and Theofilopoulos, A.N.
TITLE Immunoglobulin kappa light chain variable region gene complex
organization and immunoglobulin genes encoding anti-DNA
autoantibodies in lupus mice
JOURNAL J. Clin. Invest. 82, 852-860 (1988)
MEDLINE 88331394
COMMENT Draft entry and computer-readable sequence [1] kindly submitted by
R.Kofler 28-JUL-1988.

NCBI gi: 196949 Location/Qualifiers
source 1..462
/organism="Mus musculus"
mRNA 1..>462
/note="IgMk mRNA"
sig_peptide 52..109
/note="Ig heavy chain signal peptide"
/codon_start=1
CDS 52..>462
/note="IgMk heavy chain precursor; NCBI gi: 196950"
/codon_start=1
/translation="MGKSWIFLLSVAGHSEIQAGAEIVKPGASVKISCKAS
GYSFTCYNNHWKQSHGKSLKLEWIGNIPYGSTSYNQKFKGATLVDKSSSTAYMQL
NSLTSDSAVYYCARGNYGSSFDYWGQGTTLTVSS"
mat_peptide 110..>462
/note="Ig heavy chain"
/codon_start=1
BASE COUNT 126 a 115 c 108 g 113 t
ORIGIN Chromosome 12.

Query Match 77.0%; Score 312; DB 56; Length 462;
Best Local Similarity 94.6%; Pred. No. 4.07e-274;
Matches 331; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 52 atgggatggagctggtatcttctctctctgtcagtaactcaggtgtccactctgag 111
Qy 1 ATGGGATGAGCGGGATCTTCTCTCTCTGTGTCAGGAACCTGCACTCTCCTGAG 60
Db 112 atccagctgcagcgtctgagctgagctgggtgagcctggggttcagtgaagatacc 171
Qy 61 ATCCAGCTGCAGCAGCTGCGACCTGAGCTGATCAAGCCTGGGGCTTCAGTGAAGATATCC 120
Db 172 tgcaggctctggttactactcactcactgctcacatgaactgggtgagcagagccat 231
Qy 121 TCGAAGGCTTCTGGTTACTCTTACTAGCTATTACATACATCGGTGCAAGCAGGCCAT 180
Db 232 ggaagagccttgagtgagtggaataattactactactggtagtactagctacat 291
Qy 181 GGAAGAGCCTTGATGGATTGATATATTGATCCTTTCAATGGTGGTACTAGTACATCC 240
Db 292 cagaagttcaaggcgaaggccattgactgtagacaaatcttcacagacagcctacatg 351
Qy 241 CAGAAATTCAGCGGCGAGCCACATTGACTGTGTGACAAATCTCCAGCAGACGCTACATG 300
Db 352 cagctcaacagcctgacatctgaggaactctgcagctctattactgtgcaag 401
Qy 301 CATCTACGAGCCTGACATCTGAGGACTCTGCAGCTCTATTACTGTGCGAG 350
RESULT 2

Jul 8 08:32

US-08-137-117B-26.gp

4

LOCUS MUSIGHM195 405 bp mRNA ROD 13-AUG-1992
DEFINITION Mus musculus Ig heavy chain mRNA V-region, from hybridoma M195.
ACCESSION M83098
KEYWORDS V-region; immunoglobulin; immunoglobulin heavy chain.
SOURCE Mus musculus hybridoma M195 cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 405)
AUTHORS Co, M.S., Avdalovic, N.M., Caron, P.C., Avdalovic, M.V.,
Scheinberg, D.A. and Queen, C.
TITLE Chimeric and humanized antibodies with specificity for the CD33
antigen

JOURNAL J. Immunol. 148, 1149-1154 (1992)
MEDLINE 92148135
COMMENT NCBI gi: 195613
FEATURES Location/Qualifiers
source 1..405
/organism="Mus musculus"
/sequenced_mol="cDNA to mRNA"
/tissue_type="hybridoma M195"
sig_peptide 1..60
/gene="Igh"
/map="chromosome 12"
/note="putative"
/codon_start=1
CDS 1..405
/partial
/gene="Igh"
/map="chromosome 12"
/note="V-region; putative; NCBI gi: 195614"
/codon_start=1
/product="immunoglobulin heavy chain"
/translation="MGKSWIFLLSGTACGVHSEVQLQSGPELVKPGASVKISCKAS
GTFYTDNHHWKQSHGKSLKLEWIGIYPYNGGTGYNQKFKSKATLVDNSSTAYMDV
RSLTSDSAVYYCARGPAMDYWGQGTSTVTS"
mat_peptide 61..405
/gene="Igh"
/map="chromosome 12"
/note="V-region"
/codon_start=1
/product="immunoglobulin heavy chain"

BASE COUNT 101 a 106 c 105 g 93 t
ORIGIN
Query Match 75.8%; Score 307; DB 56; Length 405;
Best Local Similarity 88.3%; Pred. No. 4.32e-269;
Matches 354; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
Db 1 atgggatggagctggatcttctctctctcctgtcaggaactcgaggtccactctgag 60
Qy 1 ATGGGATGAGCGGGATCTTCTCTCTCTGTGTCAGGAACCTGCGAGTGTCCACTCTGAG 60
Db 61 gtccagcttcagcagctcaggaactcaggtgggtgaaacctggggcctcagtgaagatacc 120
Qy 61 ATCCAGCTGCAGCAGCTGCGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120
Db 121 tgcaggctctggatcacattactcactacacatgcactgcactgggtgagcagagccat 180
Qy 121 TGCAGGGCTTCTGGTTACTTACTTACTAGCTATTACATACACTGGGTGAGCAGGCCAT 180
Db 181 ggaagagccttgagtgagtgatattattcttacaatggtggtactggctacaac 240
Qy 181 GGAAGAGCCTTGAGTGCATGATATATTGATCCTTTCAATGGTGGTACTAGTACATCC 240

241	cagaagttcaagcaagggccacattgactgtagacaattctccagcacagcctacatg	300
241	CAGAAATTCAGGGCAAGGCCACATTGACTGTTGACAAATCTTCCGACAGCCTACATG	300
301	gaagtcacagcgcctgacatctgagagactctgagtcattactgtcaagaggggcgcccc	360
301	CATCTCAGCAGCCTGACATCTGAGACTCTGCAGTCTATTACTGTGCAAGGGGGGTAAAC	360
361	gctatggactactggggccaaggaacctcagtcaccgcgtctc	401
361	CGCTTTGCTTACTGGGGCCAAAGGACTCTGGTCTACTGTCTC	401

RESULT	3
LOCUS	S51851 421 bp DNA ROD 08-MAR-1993
DEFINITION	M104E myeloma immunoglobulin heavy chain [mice, Genomic/mRNA, 421 nt].
ACCESSION	S51851
KEYWORDS	.
SOURCE	mice.
ORGANISM	Mus sp. Unclassified.
REFERENCE	1 (bases 1 to 421)
AUTHORS	Takahashi,S., Matsumura,Y., Taniguchi,T., Tamura,H., Bitoh,S., Onishi,S., Yamamoto,Y., Yamamoto,H. and Fujimoto,S.
TITLE	Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and anti-idiotypic antibodies involved in B-B cellular interaction
JOURNAL	Microbiol. Immunol. 36 (8), 855-863 (1992)
MEDLINE	93116638
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibseq 121470] from the original journal article. This sequence comes from Fig. 1.

```

COMMENT      NCBI gi: 262657
FEATURES
  source      Location/Qualifiers
              1..421
              /organism="Mus sp."
              /note="mice"
              1..421
  CDS         /partial
              /note="Description: M104E myeloma immunoglobulin heavy
              chain"
              /codon_start=1
BASE COUNT   106 a 100 c 113 g 102 t
ORIGIN
Query Match  73.1%; Score 296; DB 59; Length 421;
Best Local Similarity 92.0%; Pred. No. 4,83e-258;
Matches 324; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

```

Db	1	atgggatgagctggatctctctctctctctctctgtcaggaaactgcaggtgtcctctctgag	60
Qy	1	ATGGGATGAGCGGGATCTTTCTCTCTCTCAGGAACTGCAGGTGCCACTCTGAG	60
Db	61	gtccagctgcacaactctgacctgagctgggtgaagcctggggcttcagtgaaagatgtcc	120
Qy	61	ATCCAGCTGCAGCAGCTGGACCTGAGCTGATGAAGCGCTGGGCTTCAGTGAAGATATCC	120
Db	121	tgtaaaggtcttgatcacaccattcaactgactactacatgaagtgggtgaacagagatcat	180
Qy	121	TGCAAGGCTTCGTGGCTTACTCATTCACTAGCTATTACATACACTGGGTGAGCAGACCCAT	180
Db	181	ggaagaagccttgatggatggagatattaatcctcaacaatggtgtagctagctacaac	240

Qy	191	GGAAAGACCTTGA	CGATTGGATATATTCATCTTCAATGGTGGTACTAGCTACAC	240
Db	241	cagaagttcaaggcg	caacattgactgtagacaaatcctccagcacagcctacatg	300
Qy	241	CAGAAATTCAGGCG	CAAGGCCACATTGACTGTGTGACAAATTCCTCAGCAGCAGCCTACATG	300
Db	301	cagctcaacagcctg	acatctgagcagctctgagctctgcagctctattactgtgcaagg	352
Qy	301	CATCTCAGCAGCTG	ACATCTGAGGACTCTCCAGTCTATTACTGTGCAAGGG	352
RESULT	4			
LOCUS		MUSHA5	440 bp mRNA	ROD 24-JUL-1991
DEFINITION			Mouse active H-chain VJ region, 5' cds.	
ACCESSION		M74138		
KEYWORDS			J-region; V-region; immunoglobulin heavy chain.	
SOURCE			Mus musculus cDNA to mRNA.	
ORGANISM			Mus musculus	
REFERENCE			Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.	
AUTHORS			1 (bases 1 to 440)	
TITLE			Rueff-Juy,D., Marche,P.N., Drapier,A.-M. and Cazenave,P.-A. Functional diversity of H and L chains allows the coexpression of two mutually exclusive idiotopes (IdI104 and IdI558)	
JOURNAL			J. Immunol. 146, 4024-4030 (1991)	
MEDLINE			91237115	
COMMENT			NCBI gi: 193746	
FEATURES			Location/Qualifiers	
source			1..440	
			/organism="Mus musculus"	
			/cell_line="hybridoma"	
			/sequenced_mol="cDNA to mRNA"	
			39..440	
			/partial	
			/note="NCBI gi: 193747"	
			/codon_start=1	
			/product="Ab 414.2 heavy chain variable and joining region"	
CDS			/translation="MEIDLSLPLVNRCLISEVLIQQSGPELVKPGASVKMSCKASQY TFDYMKVKQKSGLSLEIIGDNPYNGSTSYNGKFKGATLTVDKSSSTAYMQLINS LTSEDASVYVCARSNYTFDYGQGTTLVSS"	
BASE COUNT			119 a 113 c 104 g 104 t	
ORIGIN				

	72.1%;	Score 292;	DB 55;	Length 440;
Query Match	88.6%;	Pred. No. 4..99e-254;		
Best Local Similarity	0;	Mismatches 42;	Indels 4;	Gaps 3;
Matches 358; Conservative				
D _b	34	atgggatggaactggatctttctctccttcttcaggaacctcgagggtgcct-ctctgag	92	
Oy	1	ATGGGATGGAGCGGGATCTTTCCTTCCTTCGTGAGGAACTCGAGTGTCACACTCGAG	60	
D _b	93	gtccagt-gcaacaacatcggaacctggagctggagtgggtgaagccctggggcttcagtgaagatgcc	152	
Oy	61	ATCCAGCTGCCAGCAGCTGCAGCTGCAGCTGATGAAGCGTTGGGCTTCAGTCAAGAATATCC	120	
D _b	153	tgtaaaggttgttgatacacattcaactgactactacatgaagtgggtgaagcagagaccat	212	
Oy	121	TCCAAGGCTTCTGGTTACTATTCACTAGCTATTATACAACACTGGGTGAGCAGAGCCAT	180	
D _b	213	ggaagaagccttgagtggattggagatatctaactccaacaggtggttaactagctaacac	272	
Oy	181	GGAAGAGCGCTTCGAGTGGATTTGGATTAATTGATCTTCATTCCTTTCAA TGSTGGTAGCTACAA C	240	

Jul 8 08:32

US-08-137-117B-26.rgs

11

```
Qy 181 GCAAGAGCGCTGAGTGGATTGGATATATTGATCTTTCAAATGGTGGTACTAGCTACAAC 240
|||||
Db 241 cagaagtcaagggttaagccaccattgaactagacaaagtcctccagcacagcctacatg 300
|||||
Qy 241 CAGAAATTCAGGGCAAGGCCACATTGACTGTTGACAAATCTTCCAGCAGCCTACATG 300
|||||
Db 301 gaactccgagcctgacatctgaggaactcgagctctattactgtgc 347
|||||
Qy 301 CATCTCAGCAGCGCTGACATCTGAGGACTCTGCGAGTCTATTACTGTGC 347
|||||
```

```
RESULT 9
LOCUS MD1GMVAV 348 bp RNA ROD 01-APR-1993
DEFINITION M.domesticus IgM variable region.
ACCESSION 222095
KEYWORDS anti-DNA antibody; IgM gene; IgM variable region; immunoglobulin.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus
Eukaryote; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
1 (bases 1 to 348)
Tillman,D.M., Jou,N., Hill,R.J. and Marion,T.N.
Both IgM and IgG anti-DNA antibody are the products of clonally
selective B cell stimulation in (NZB x NZW)F1 mice
J. Exp. Med. (1992) In press
2 (bases 1 to 348)
Marion,T.N.
Direct Submission
```

```
REFERENCE Submitted (23-MAR-1993) to the EMBL/GenBank/DBJ databases. Tony N.
Marion, Microbiology and Immunology, University of Tennessee,
Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA
NCBI gi: 288723
```

```
FEATURES
source
1..348
/organism="Mus domesticus"
/strain="(NZB x NZW)F1"
/dev_stage="somatic variant"
/tissue_type="spleen"
/cell_type="hybridoma"
/cell_line="17s.166"
/isolate="mouse #17"
/chromosomes="12"
/sex="Female"
<1..>348
/gene="IgM"
/notes="NCBI gi: 288724"
/codon_start=1
/function="heavy chain variable region for IgM anti-DNA
antibody; Vh558 family"
/product="immunoglobulin variable region"
/translation="EVQLQQSGPELVKPGASVKISCKASGYFSGYIMHWKQSPKES
LEWIGEINPSTGITTNQKFKAKATLTVDKSSSTAYMQLKSLTSDSAVYVCARGRYT
FAYWGQCLTVTVA"
```

```
BASE COUNT 89 a 81 c 94 g 83 t 1 others
ORIGIN
Query Match 69.68; Score 282; DB 53; Length 348;
Best Local Similarity 90.28; Pred. No. 5.31e-244;
Matches 314; Conservative 1; Mismatches 33; Indels 0; Gaps 0;
```

Jul 8 08:32

US-08-137-117B-26.rgs

12

```
Db 1 gaggtccagctgcagcagctctggacctgagctgggtgaagcctggggttcagtgaaata 60
|||
Qy 58 GAGATCCAGCTCGACGAGCTCGACCTGAGCTGATGACGCTGGGGCTTCAGTGAAGATA 117
|||||
Db 61 tctgtcaaggcttctgttactcattcactggctactacatgcactgggtgaagcaagt 120
|||||
Qy 118 TCCTGCAAGGCTTCTGTTACTCTATTCTAGTATTATACATACACTGGGTGAAGCAGCG 177
|||||
Db 121 cctgaaaagagccttgagtgattggagagattaatcctagcactgggtgtattacttac 180
|||||
Qy 178 CATGGAAGACGCTTGAGTGGATTGGATATTATTCCTTCAATGGTGGTACTAGTAC 237
|||||
Db 181 aaccagaagttcaaggccaagccacattgactagacaaatcctccagcacagcctac 240
|||||
Qy 238 AACACGAATTCAGGGCAGGCCACATTGACTCTTGACAAATCTTCACAGCACAGCCTAC 297
|||||
Db 241 atgcagctcaagagcctgacatctgaggactctgcagctctattactgtcagagaggag 300
|||||
Qy 298 ATGCATCTCAGCAGCGCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGGGGGT 357
|||||
Db 301 tatactttgcttactggggccaaggagctctggtcactgtctctgca 348
|||
Qy 358 AACCGCTTTGCTTACTGGGGCAAGGGACTCTGGTCACTGCTCTGCA 405
|||||
```

```
RESULT 10
LOCUS M1SHA4 440 bp mRNA ROD 24-JUL-1991
DEFINITION Mouse active H-chain VJ region, 5' cds.
ACCESSION M74137
KEYWORDS J-region; V-region; immunoglobulin heavy chain.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
Eukaryote; Animlia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 440)
Rueff-Juy,D., Marche,P.N., Drapier,A.-M. and Cazenave,P.-A.
Junctional diversity of H and L chains allows the coexpression of
two mutually exclusive idiotopes (Id1104 and Id1558)
J. Immunol. 146, 4024-4030 (1991)
```

```
JOURNAL 91237115
MEDLINE
COMMENT NCBI gi: 193744
FEATURES Location/Qualifiers
source
1..440
/organism="Mus musculus"
/cell_line="hybridoma"
/sequenced_mol="cDNA to mRNA"
39..440
/partial
/notes="NCBI gi: 193745"
/codon_start=1
/product="Ab 16.3 heavy chain variable and joining
regions"
/translation="MELDLSPIVRNCRCLSEVQLQQSGPELVKPGASVKMSCKASGY
TFDYIMHWKQSPCKSLEWIGDISPNNGCTSINQKFKKATLTVDKSSSTAYMQLNS
LTSEDSAVYVCARDYDWFVWGVTGTVTVSS"
```

```
BASE COUNT 114 a 112 c 110 g 104 t
ORIGIN
Query Match 69.4%; Score 281; DB 55; Length 440;
Best Local Similarity 90.9%; Pred. No. 5.33e-243;
Matches 318; Conservative 0; Mismatches 31; Indels 1; Gaps 1;
Db 34 atgggatgagctgagctcttctctctctctgctcaggaactgcaggtgtct-ctctgag 92
|||||
```

```
Qy 1 ATGGGATGAGCGGGATCTTCTCTCTCTGTCAGAACTGACGAGTGTCCACTCTGAG 60
Db 93 gtccagctcaacaatcgacctgagctgggtaaagcctggggtctcagtgaaagtctcc 152
||||| ||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||
Qy 61 ATCCAGCTGCAGCAGTCTGGAGCTGACCTGATGAAGCTGGGGCTTCAGTGAAGATATCC 120
||||| ||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||
Db 153 tgaagctcttgatcacacattcaactgactactacatgaagtgggtgaagcagagcct 212
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
Qy 121 TCGAAGCTTCTGCTTACTTACTTCACTAGCTATTACATAGCTGGTGAAGCAGACCATG 180
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
Db 213 ggaagagccttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 272
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
Qy 181 CGAAGAGGCTTGAGTGATGGATATATGATCCCTTCAATGGTGGTACTAGCTACAAC 240
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
Db 273 cagaagtcgaagggaagccacattgactgactgactgactgactgactgactgactgactg 332
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
Qy 241 CAGAAATTCAGAGGCAAGGCGACATTGACTGTGGACAAATCTTCAGCAGACGCTACATG 300
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
Db 333 cagctcaacagccttacatctgagtgactctgagtgactctgagtgactctgagtgactg 382
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
Qy 301 CATCTCAGCAGCCTGACATCTGAGACTCTGCAGCTATTACTGCTGCAAG 350
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||

RESULT 11
LOCUS A07953 450 bp RNA PAT 01-SEP-1993
DEFINITION Artificial sequence for anti-hcG antibody.
ACCESSION A07953
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
REFERENCE 1 (bases 1 to 450)
AUTHORS van Wezenbeek, P.M.G.F. and Bos, E.S.
TITLE Anti-hcG antibodies
JOURNAL Patent: EP 0370581-A 9 30-MAY-1990;
ARKZO N.V.
COMMENT NCBI gi: 411512
FEATURES
source location/Qualifiers
1..450
/organism="Artificial sequences"
39..>450
/notes="NCBI gi: 411513"
/codon_start=1
/product="anti-hcG antibody"
/translation="MGMSEWIFLLSGTAGVHSEVQLQSGPELVKPGASVKISKAS
GYFTDYNHVKQSHGRSLIEWIGYIPYSGPTGYNQRENSKATLTVDNSSSTAFMEV
RSLTSEDSAVYVCARECIFYMDYHQQGTSVTSS"
BASE COUNT 116 a 116 c 113 g 105 t
ORIGIN
Query Match 68.9%; Score 279; DB 33; Length 450;
Best Local Similarity 87.8%; Pred. No. 5.37e-241;
Matches 324; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 39 atgggatggagctgtcttctctctctctctctctcaggaactgcaggcgtccactctgag 98
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Qy 1 ATGGGATGAGCGGGAATCTTCTCTCTCTCTGTCAGGAAGTCTGAGTCTGCACTCTCAG 60
||||| ||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||
Db 99 gtccagctcaacagtcaggacctgagctggtgaaacctggcgctcagtgaaagatccc 158
||||| ||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||
Qy 61 ATCCAGCTGCAGCAGTCTGCACTGAGCTGAGTGAAGCCTGGGGCTTCAGTGAAGATATCC 120
||||| ||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||
Db 159 tgaagctcttgatcacacattcaactgactgactgactgactgactgactgactgactg 218
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
```

```
Qy 121 TCGAAGCTTCTGCTTACTTACTTCACTAGCTATTACATACACTGGGTGAAGCAGCCAT 180
Db 219 ggaagcagccttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 278
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Qy 181 GGAAGACGCCCTTGAGTGGATATATGATCCTTTCAATGGTGGTACTAGCTACAAC 240
||||| ||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||
Db 279 cagaggttcaacagcaagccacattgactgactgactgactgactgactgactgactgactg 338
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
Qy 241 CAGAAATTCAGAGGCAAGGCGACATTGACTGTTCAGAAATCTTCAGCAGCAGCCTACATG 300
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
Db 339 gaggtccagcagcctgacatctggaagactctcagctctcagctctcagctctcagctctcag 398
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||
Qy 301 CATCTCAGCAGCCTGACATCTGAGGACTCTGAGGACTCTGAGTCTATTACTGCAAGGGGGGTAAC 360
||||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| ||| ||||||| |||

Db 399 ttctatact 407
|||||
Qy 361 CGCTTTGCT 369

RESULT 12
LOCUS MDICNVBC 348 bp RNA ROD 05-NOV-1994
DEFINITION M.domesticus IgM variable region.
ACCESSION 222136
KEYWORDS anti-DNA antibody; IgM gene; IgM variable region; immunoglobulin.
SOURCE western European house mouse.
ORGANISM Mus musculus domesticus
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;
Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 348)
AUTHORS Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
TITLE Both IgM and IgG anti-DNA antibodies are the products of clonally
selective B cell stimulation in (NZB x NZW)F1 mice
JOURNAL J. Exp. Med. 176 (3), 761-779 (1992)
MEDLINE 92381444
REFERENCE 2 (bases 1 to 348)
AUTHORS Marion,T.N.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-1993) to the EMBL/GenBank/DBJ databases. Tony N.
Marion, Microbiology and Immunology, University of, Tennessee,
Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA
COMMENT NCBI gi: 297745
FEATURES
source location/Qualifiers
1..348
/organism="Mus domesticus"
/strain="(NZB x NZW)F1"
/dev_stage="somatic variant"
/tissue_type="spleen"
/cell_type="hybridoma"
/cell_line="25.12"
/isolate="mouse #25"
/chromosome="12"
/sex="Female"
<1..>348
/gene="IgM"
/notes="NCBI gi: 297746"
/codon_start=1
/function="heavy chain variable region for IgM anti-DNA
antibody; VH558 family"
/product="immunoglobulin variable region"
/translations="QVQLQQSDRELIVKPKSVKISKASGYFTDYNMDWVKQSHCKS
LEWIGYIPNNGGTGINOKFKSKATLTVDKSSSTATYMEHLISLTSSEDSAVYTCARGRYT
```

```
BASE COUNT      91 a   82 c   94 g   80 t   1 others
ORIGIN
FAYWCGCTLVTVSA"
Query Match      68.6%; Score 278; DB 53; Length 348;
Best Local Similarity 89.9%; Pred. No. 5.39e-240;
Matches 312; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Db 2 aggtccagctgcagcagctgacgctgagctggtgaagcctggngcttcagtgaaagtat 61
|||
Qy 59 AGATCCAGCTGCACGACTCTGACCTGACCTGACCTGATGAAGCCTGGGCTTCAGTGAAGTAT 118
|||
Db 62 cctcgaagcttctggataccatttcactgactacaacatggactgggtgaagcagagcc 121
|||
Qy 119 CCTGGAAGGCTTCTGGTACTCATCTAGCTATTACATACACTGGGTGAGCAGAGCC 178
|||
Db 122 atgaaagagccttgagtgagtgatattatctctaacaatgggtggtactggctaca 181
|||
Qy 179 ATGGAAGAGCGCTTCTAGTGGATTGATATTATTCCTTTCAATGGTGGTACTAGCTACA 238
|||
Db 182 accaagaagtcaagagcagcagcattgactgtagacaagtcctccagcagagcctaca 241
|||
Qy 239 ACCAGAAATTCAGGGCAAGGCCACATTGACTGTTGCAAAATCTTCCAGCAGACCTACA 298
|||
Db 242 tggagctccacagcctgacatctgagcactgtgcagctctattactgtgcaagggaggt 301
|||
Qy 299 TGCATCTCAGCAGCGCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGGGGGTA 358
|||
Db 302 atacgtttgttactggggcgaaggactctggtcactgtctctgca 348
|||
Qy 359 ACCGCTTGTCTACTGGGGCCAGGGACTCTGGTCACTGTCTGTCCA 405
|||

RESULT 13
LOCUS MUSIGHZF 2908 bp DNA ROD 25-JUL-1991
DEFINITION Mouse Ig rearranged heavy chain gene V205.12-D-J region, hybridoma
A20/44.
ACCESSION M58535
KEYWORDS V-region; immunoglobulin heavy chain.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 2908)
AUTHORS Both,G.W., Taylor,L., Pollard,J.W. and Steele,E.J.
TITLE Distribution of mutations around rearranged heavy-chain antibody
variable-region genes
JOURNAL Mol. Cell. Biol. 10, 5187-5196 (1990)
MEDLINE 90377208
COMMENT NCBI gi: 196346
FEATURES
source 1..2908
/organism="Mus musculus"
/strain="C57BL/6J"
/sub_species="domesticus"
/sequenced_mol="DNA"

BASE COUNT      825 a   555 c   676 g   850 t   2 others
ORIGIN

Query Match      68.6%; Score 278; DB 56; Length 2908;
Best Local Similarity 90.1%; Pred. No. 5.39e-240;
Matches 329; Conservative 0; Mismatches 33; Indels 3; Gaps 2;

Db 756 caggtgtctctctcgtggtccagctgcaacaatctggacctgaacgggtgaagcctgggg 815
```

```
Qy 44 CAGGTGTCACCTCTGAGATCCAGCTGCAGCAGTCTGGACCTGAGCTGATGAAGCCTGGGG 103
|||
Db 816 cttcagtgagatttcctgaagcttctggatacacgttccactgactactacatgaact 875
|||
Qy 104 CTTCACTGAGATATCTCTGCNAGGCTTCTGTTACTTCATTCACCTAGCTATTACATACACT 163
|||
Db 876 ggtgaaacagagcaatggaagagccttgagtgagtggtggagatattaatcctaacaatg 935
|||
Qy 164 GCGTGAAGCAGACCATGGAAGAGCGCTTGAGTGGATTGGATATATTGATCTTTCAATG 223
|||
Db 936 gtggtactagtacaaccagaagttcgaggggcgaaggccacattgactgtagacaagtcct 995
|||
Qy 224 GTGTACTAGCTACAACAGAAATTCAGGGCAAGGCCACATTGACTGTTGACAAATCTT 283
|||
Db 996 ccagcagcctacatggagctccgcagctgacatctgaggactctgcagctcagctattact 1055
|||
Qy 284 CCAGCAGCCCTACATGCTCAGCAGCCTGACATCTGAGGACTCTGAGCTCTATTACT 343
|||
Db 1056 gtgcaagaggggattacactggtttccttactggggccaaaggactctggtcactgtct 1115
|||
Qy 344 GTGCAAGGGGGGG--TA-ACCGCTTTGCTTACTGGGGCCAGGGCACTCTGGTCACTGTCT 400
|||
Db 1116 ctgca 1120
|||
Qy 401 CTGCA 405
|||

RESULT 14
LOCUS MUSIGHFX 412 bp mRNA ROD 15-MAR-1990
DEFINITION Mouse Ig family J558 active mu-chain V-J3 region anti-dextran mRNA,
hybridoma 9.14.7.
ACCESSION M17724
KEYWORDS C-region; J-region; V-region; immunoglobulin heavy chain;
immunoglobulin mu-chain; processed gene.
SOURCE Mouse (BALB/c) hybridoma cell line 9.14.7., cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE 1 (bases 1 to 412)
AUTHORS Akolkar,P.N., Sikder,S.K., Bhattacharya,S.B., Liao,J., Gruero,F.,
Morrison,S.L. and Kabat,E.A.
TITLE Different V-L and V-H germ-line genes are used to produce similar
combining sites with specificity for alpha-(1->6) dextrans
JOURNAL J. Immunol. 138, 4472-4479 (1987)
MEDLINE 87224123
REFERENCE 2 (bases 1 to 56)
AUTHORS Akolkar,P.N., Sikder,S.K., Bhattacharya,S.B., Liao,J., Gruero,F.,
Morrison,S.L. and Kabat,E.A.
TITLE Errata: Different V-L and V-H germ-line genes are used to produce
similar combining sites with specificity for alpha-(1->6) dextrans
JOURNAL J. Immunol. 139, 3911-3911 (1987)
COMMENT [2] revises [1].

FEATURES
source NCBI gi: 195313
Location/Qualifiers
1..412
/organism="Mus musculus"
<1..55
eig_peptide /note="Ig mu heavy chain V-J3-region signal peptide"
/codon_start=2
<1..3412
CDS /note="Ig mu heavy chain V-J3-region; NCBI gi: 195314"
/codon_start=2
```

/translation="KSWIFLFXLLSCTAGVLSEVQLQSGPELVKPGASVKISKASG
YFTDTYIMKWVSHGSHKLEIGDINPNNGTSYNOKRKAFLFDKSSSTAYMQLN
SLTSEDSAVYYCARDYYGSSSFYMQGGLTVTSV"

mat_peptide 56..>412

/note="Ig mu heavy chain V-J3-region"

/codon_start=1

BASE COUNT 105 a 94 c 105 g 105 t 3 others

ORIGIN Chromosome 12.

Query Match 67.4%; Score 273; DB 56; Length 412;
Best Local Similarity 91.1%; Pred. No. 5.47e-235;
Matches 317; Conservative 0; Mismatches 28; Indels 3; Gaps 2;

Db 1 atggagctgagatctttctcttctnnmctctgtcaggaaactcgaggtctcctctctgaggt 60
Qy 6 ATGGAGCGGGATCTTCTCTTCC--TCT-GTCAAGAACTGCGAGGTCTCCACTCTGAGAT 62
Db 61 ccaagtgcacaatctggacctgagctggtgaagcctggggcctcaagtgaagatatcctg 120
Qy 63 CCAGCTGCAGCAGTCTGGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAACATATCTG 122
Db 121 taaggtcttgatcacattcactgactactacatgaagtgggtgaagcagagtcatgg 180
Qy 123 CAAAGCTCTGTGTTACTCATTCACTACACTATTACATACACTGGCTGAAGCAGCGCATGG 182
Db 181 aaagagccttgagtggtggtgagatataactcaacaatggtggtactagtcacaacca 240
Qy 183 AAGAGCGCTTGAGTGGATGGATATATTGATCCTTTCATGGTGGTACTAGCTACACCA 242
Db 241 gaagtcaaggccaagccacatgactgtagacaaatcctccagcacagcctacatgca 300
Qy 243 GAAATTCAGGGCAAGGCCACATGACTGTTGACAAATCTTCCAGCAGCGCTACATGCA 302
Db 301 gctcaacagcctgacatctgagagactctgcagtctattactgtgcaag 348
Qy 303 TCTCAGCAGCCTGCATCTGAGACTCTGCAGCTCTGCAGCTATTACTGTGCAAG 350

RESULT 15
LOCUS I05341 414 bp DNA PAT 14-NOV-1994
DEFINITION Sequence 3 from patent EP 0256654.
ACCESSION I05341
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 414)
AUTHORS Schoemaker,H.J. and Sun,L.K.
TITLE Chimeric rodent/human immunoglobulin specific for tumour-associated antigens
JOURNAL Patent: EP 0256654-A2 3 24-FEB-1988;

COMMENT NCBI gi: 591098
FEATURES Location/Qualifiers
source 1..414
/organism="unknown"
BASE COUNT 96 a 97 c 115 g 106 t
ORIGIN

Query Match 67.4%; Score 273; DB 35; Length 414;
Best Local Similarity 83.7%; Pred. No. 5.47e-235;
Matches 339; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Db 10 atggaatggagcagagctttcttctctctctctctctctctctctctctctctctctccag 69

Qy 1 ATGGGATGGAGCGGGATCTTCTTCTTCCTTCTGTGAGGAAGTGCAGGTTGCCACTCTGAG 60
Db 70 gtccagttgcagcagctctggagctgagctggtgaagcctgggacttcagttcagtgaaagtgtcc 129
Qy 61 ATCCAGCTGCAGCAGCTCTGGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAACATATCC 120
Db 130 tgaaggctctctgatacagccttcactaattacttgatagagtggtggttaaacagagagcct 189
Qy 121 TGAAGGCTTCTGGTTACTCATTACTAGCTATTACATACACTGGGTGAAGCAGGCCAT 180
Db 190 ggacaggccttgagtggaattggggtgattaatcctgggaagtggtggtactaaactacaat 249
Qy 181 GAAAGAGCCTTCAGTGGATTGGATATATTGATCCTTTCAATGGTGTACTAGCTACAAC 240
Db 250 gagaagttcaaggccaaggaacaactgactgcagacaatacctccagcaactgcctacatg 309
Qy 241 CAGAAATTCAGGGCCAGGCCACATTGACTGTTGACAAATCTTCCAGCACAGCCTACATG 300
Db 310 cagctcagcagcctgacatctgatgactctgcggtctctattctgtgcaagagatggtccc 369
Qy 301 CATCTCAGCAGCCTGCATCTGAGGACTCTGCAGTCTATTACTGTCAAGGGGGGTAAC 360
Db 370 tggtttgcttaactggggccaaggagactctggtcaactgtctctgca 414
Qy 361 CGCTTTGCTTACTGGGGCCAAAGGACTCTGGTCACTGCTCTGCA 405

Search completed: Mon Jul 8 08:43:12 1996
Job time : 286 secs.

.....

(MT)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligenetics, Inc.

MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

```
Run on: Mon Jul 8 08:43:30 1996; MasPar time 35.45 Seconds
759.603 Million cell updates/sec
```

Tabular output not generated.

Title: >US-08-137-117B-26

Description: (1-405) from US08137117B.seq

Perfect Score: 40

N.A. Sequence: 1 ATGGGATGGAGCGGATCTT.....CTCTGGTCACTGTCTCTGCA 405

Comp: TACCCTACCTCGCCCTAGAA.....GAGACCAGTGACAGAGACGT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 84802 seqs. 33246950 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-nenesen22

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 8.356: Variance 5.470: scale 1.528

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description	Pred. No.
		Match	Length					
1	403	99.5	405	5	Q30754	p12-h2.	1.82e-238	
2	301	74.3	443	11	Q45428	KM-750 heavy chain.	2.77e-172	
3	293	72.3	449	11	Q45426	KM-796 heavy chain.	4.11e-167	
4	280	69.1	474	2	Q12098	Sequence encoding hea	1.02e-158	
5	280	69.1	474	2	Q12014	Sequence encoding mou	1.02e-158	
6	279	68.9	450	1	Q04695	Heavy chain variable	4.49e-158	
7	269	66.4	420	11	Q68700	DRG-200 Ab heavy cha	1.26e-151	
8	268	66.2	471	5	Q08607	Co-1 Heavy Chain V Re	5.56e-151	
9	267	65.9	499	2	Q11291	Encodes murine monoc	2.45e-150	

PT Reconstituted human antibody to human interleukin-6 receptor -

Jul 8 08:33

US-08-137-117B-26.mg

5

Qy 301 CATCTCAGGAGCTGACATCTCAGGACTCTGCAGCTCTATTACTGTGCAAG-G-GGGG-GT 357
Db 393 tattactaacgctgggactggggcgaaggagactctggtcaactgtctctgca 443
Qy 358 AACCGCTTTCCTT---ACTGGGGCAAGGAGCTCTGGTCACTGTCTCTGCA 405

RESULT 3
ID Q45426 standard; cDNA; 449 BP.
AC Q45426;
DT 17-NOV-1994 (first entry)
DE KM-796 heavy chain.
KW Monoclonal antibody; Ab; ganglioside GM2; chimera;
KW chimeric antibody; expression vector; heavy; light; chain;
KW hypervariable region; CDR; constant region; hybridoma;
KW Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 33..449
FT /*tag= a
FT /note= "excluding stop codon"
FT sig_peptide 33..89
FT /*tag= b
FT /note= "sig_peptide"
FT misc_feature 180..194
FT /*tag= c
FT /note= "hypervariable region 1;
FT claim 8"
FT misc_feature 237..287
FT /*tag= d
FT /note= "hypervariable region 2;
FT claim 8"
FT misc_feature 384..416
FT /*tag= e
FT /note= "hypervariable region 3;
FT claim 8"
FN A09346181-A.
PD 17-MAR-1994.
PE 07-SEP-1993; 046181.
PR 07-SEP-1992; JP-238452.
PA (KYOW) KYOWA HAKKO KOCYO KK.
PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
PI Shitara K;
DR MPI; 94-126957/16.
DR P-PSDB; R53328.
PT Humanised antibody specific for ganglioside GM2 - used for
PT producing a cytotoxic effect on cancers such as melanoma,
PT neuroblastoma and glioma.
PS Claim 5; Page 104-105; 191pp; English.
CC Chimeric human Ab expression vectors are constructed by inserting
CC the Ab heavy and light chain variable region-encoding cDNA
CC isolated from hybridomas producing a mouse or rat monoclonal Ab
CC reacting with the ganglioside GM2 respectively into an expression
CC vector for use in animal cells which contains the human Ab heavy and
CC light chain constant region-encoding cDNA. The expression vectors
CC are introduced into animal cells and the transformant thus obtained
CC is cultured for the prodn. of a chimeric human Ab reacting with the
CC ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric
CC human Abs will not cause anti-mouse Ig Ab prodn. in the patient's
CC body but show a prolonged blood half-life, with a reduced frequency
CC of adverse effects, so that it can be expected to be superior
CC to mouse monoclonal Abs in the efficacy in the treatment of human
CC cancer, for instance.

Jul 8 08:33

US-08-137-117B-26.mg

6

CC Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603
CC heavy and light chain sequences are given in Q45426-30.
CC CDR regions for use in chimeric Abs are indicated in the
CC Features Table.
SQ Sequence 449 BP; 108 A; 116 C; 113 G; 112 T;
Query Match 72.3%; Score 293; DB 11; Length 449;
Best Local Similarity 92.2%; Pred. No. 4.11e-167;
Matches 320; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
Db 33 atgggatggagctggatctttctctctctctctgtcaggaaactgcagggtgtcctctctgag 92
Qy 1 ATGGGATGGAGCGGATCTTCTGAG 60
Db 93 gtccagctgcagcagctctggacctgcagctgcagctgcagctgcagctgcagctgcagctgcag 152
Qy 61 ATCCAGCTGCAGCAGCTCTGCACCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGTATCC 120
Db 153 tgcagggtctctggatcacattactactactactactactactactactactactactactactact 212
Qy 121 TGCAGGCTTCTGTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTAC 180
Db 213 ggaagagccttgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 272
Qy 181 GGAAGAGCGCTTGAGTGGATATGATATGATATGATATGATATGATATGATATGATATGATATG 240
Db 273 cagaagtcgaagcgaagccac 332
Qy 241 CAGAAATTCAGAGCGCAAGGCCACATTTGACTGTTTTCACAAATCTTCCAGCACAGCCTACATG 300
Db 333 gagctccacagcctgcacatctgcagcctgcagcctgcagcctgcagcctgcagcctgcagcctgc 379
Qy 301 CATCTCAGCAGCCTGCATCTCAGGACTCTGCAGCTCTGCAGCTCTATTACTGTGC 347

RESULT 4
ID Q12058 standard; DNA; 474 BP.
AC Q12058;
DT 15-AUG-1991 (first entry)
DE Sequence encoding heavy chain variable region of murine
DE 2G12 immunoglobulin.
KW Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 52..474
FT /*tag= a
FT /product= mouse MAb 2G12 H-chain variable region
FN M09107493-A.
PD 30-MAY-1991.
PE 13-NOV-1990; U06615.
PR 13-NOV-1989; US-433730.
PA (XOMA-) XOMA CORP.
PA (GREC) GREEN CROSS CORP.
PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
DR MPI; 91-178044/24.
DR P-PSDB; R12356.
PT New chimeric mouse-human antibodies - used to detect, kill and
PT remove HIV-1 antigen from sample
PS Disclosure; fig 7; 107pp; English.
CC This sequence encodes the heavy chain variable (V) region of a
CC mouse monoclonal antibody (MAb), 2G12, specific for an HIV-1
CC viral antigen. It is used in the construction of a chimeric MAb
CC comprising heavy and light chains having murine V regions and human
CC C regions. The chimeric MABs are more effective than murine MAB

2G12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric Mabs can be used as immun-conjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV.

See also 012056-57 and 012058-63

[illegible]

RESULT	5
ID	Q12014 standard; DNA; 474 BP.
AC	Q12014;
DT	19-AUG-1991 (first entry)
DE	Sequence encoding mouse MAb 2G12 H chain V region.

OS	Mus sp.	Location/Qualifiers
FT	CD5	52..474
FT	/*tag= a	
PN	W09107494-A.	
PD	30-MAY-1991.	
PF	13-NOV-1990; U06627.	
PR	13-NOV-1989; US-433703.	
PA	(XOMA-) Xoma Corp.	
PI	Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;	
PT	WPI; 91-178106/24.	
DR	p-P5DB; R12234.	
PT	PT New chimeric mouse human antibodies - used in treatment, diagnosis	
PT	and prophylaxis of HIV infections.	
PS	Disclosure; Fig 7; 108pp; English.	
CC	The mouse VH gene product may be used to produce chimeric mouse-	

CC human Abs against HIV-1 comprising human Ig constant regions and
CC murine variable regions. These novel sequence are useful in
CC treatment, diagnosis and prophylaxis of HIV infections, and may be
CC produced by a bacterial, yeast or mammalian expression system.
SQ Sequence 474 BP; 123 A; 118 C; 112 G; 121 T

Query Match	69.1%;	Score 280;	DB 2;	Length 474;
Best local Similarity	88.5%;	Pred. No. 1.02e-158;		
Matches 322;	Conservative 0;	Mismatches 42;	Indels 0;	Gaps 0;

Db	52	atgggatgagctggatctctttctctctctctcgaagactgcaggtgctctctctgag	111
Qy	1	ATGGGATGGAGGGGATCTTTCTCTCTCTCTCTCAGGAACTCGAGGTGCCACTCTGAG	60
Db	112	gtccagctgcaacagctgtggacctggaactggtgaagctggggcttcagtggaagatctc	171
Qy	61	ATCCAGCTCGACGAGCTGGCACTGAGCTGATGAAGCTGGGGCTTCAGTGAAGATATCC	120
Db	172	tgcagagactcttgatacacattcaactgaatacacattcaactgggtgaagcagagaccat	231
Qy	121	TGCAGGCTTCTGGTTACTTCATTCACTAGCTATTACATCACTGGGTCGACGAGGCCAT	180
Db	232	ggacagagccttgagtgagtgaggattaatctcaaatgggtggtactacctacaac	291
Qy	181	GGAAAGAGCCTTGAGTGGGATATATTTGATTCCTTTCAATGGTGTGCTACTGCTACAA	240
Db	292	cagaagttcaaggaagcaggccacattgattgtagacaagctctccagcagagcctacatg	351
Qy	241	CAGAAATTCAAGGCAAGGCCACATTCACCTGTTGACAAATCTTCCAGACAGAGCCTACATG	300
Db	352	gaactccgagcctgcacactgattctgactcttactactgctgcaagaagagaaat	411
Qy	301	CATCTCAGCAGCCTCACATCTCGAGACTCTGCAGTCTATTACTGTGCAAGGGGGGGTAAC	360
Db	412	ctct	415
Qy	361	ccct	364

RESULT	6	
ID	Q04695	standard; DNA; 450 BP.
AC	Q04695;	
DT	04-OCT-1990	(first entry)
DE	Heavy chain variable domain of human chorion gonadotrophin-binding pptd.	
KW	Human chorionic gonadotropin; antibodies; heavy chain; choriocarcinoma;	
KW	abortion; tumour detection; complementary determining regions;	
KW	pregnancy prevention; ss.	
OS	Mus musculus.	
Key	Location/Qualifiers	
FN	CD5	39..449
FT	/*tag= a	
FT	/product=hCG-binding protein heavy chain variable region	
FT	misc_feature	187..200
FT	/*tag= b	
FT	/product=CDR	247..293
FT	misc_feature	
FT	/*tag= c	
FT	/product=CDR	390..416
FT	misc_feature	
FT	/*tag= d	
FT	/product=CDR	1..6
FT	misc_feature	
FT	/*tag= e	
FT	/label=EcoRI-linker	

Jul 8 08:33

US-08-137-117B-26.mg

9

PN EP-370581-A.
PD 30-MAY-1990.
PF 21-NOV-1989; 202951.
PR 25-NOV-1988; NL-002902.
PA (AIKU) AKZO NV.
DR van Wezenbeek PM;
WI 1; 90-165307/22.
DR P-PSDB; R05090.
PT Polypeptide(s) which specifically bind human chorionic gonadotropin -
contg. antigen-binding domains comprising complementary
determining domains.
PS Disclosure; P; English.
CC The variable fragment was isolated from an anti-hCG-producing
myeloma cell line. Together with the heavy chain variable domain
CC (Q04694) the sequence forms a hCG-binding antibody encoding fragment
CC (PhCG). For the production of antibodies the variable region was fused
CC to a constant region of human origin. The product can be used to prevent
CC pregnancy, for combatting choriocarcinomas or other hCG-producing tumours
CC They also have diagnostic applications as immune reagents for in vivo
CC diagnosis, eg for localisation of tumours and for in vitro diagnosis for
CC detection of hCG in body fluids.
SQ Sequence 450 BP; 116 A; 116 C; 113 G; 105 T;

Query Match 68.9%; Score 279; DB 1; Length 450;
Best Local Similarity 87.8%; Pred. No. 4.49e-158;
Matches 324; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 39 atgggagtgagtgatctttcttctctctgtcaggaaactgcagggtccactctgag 98
|||||
Qy 1 ATGGGATGAGCGGGATCTTCTCTCTCTCTCAGGAACTGCGAGGTGCCACTCTGAG 60
|||||
Db 99 gtccagcttcaacagtcaggacgtgagctgtgtgaaacctggggcctcagtgaaagatccc 158
|||||
Qy 61 ATCCAGCTGCACAGCTGTGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120
|||||
Db 159 tccaagctcttgatcacattcactgactacacatgcactgggtgaagcagagccat 218
|||||
Qy 121 TCGAAGGCTTCGTGTTACTATTACTAGCTATTACATACATGGGTGAAGCAGAGCCAT 180
|||||
Db 219 gaagagccttgagtgattggatatattatccttacagtggtcctactggctacaac 278
|||||
Qy 181 GGAAGAGCCTTCAGTGGATTGGATATATTGATCCTTTCAATGGTGGTACTACTACAAC 240
|||||
Db 279 cagaggttcaacagcaagggccacattgactgtagacaattcctccagcagagccttcag 338
|||||
Qy 241 CAGAAATTCAGGGCAAGGCCACATTGACTGTGTGACAAATCTTCCAGCAGACGCTACATG 300
|||||
Db 339 gagggtccgagcctgacatctgaagactctgagctctattactgtgcaagagaggggac 398
|||||
Qy 301 CATCTCAGAGCGCTGCATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGGGGGTAC 360
|||||
Db 399 ttcttact 407
Qy 361 CGCTTTGCT 369

RESULT 7
ID Q66700 standard; cDNA; 420 BP.
AC Q66700;
DT 16-NOV-1994 (first entry)
DE DREG-200 Ab heavy chain variable region.
KW DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1;
humanized antibody; immunoglobulin; Ig; IgG1; IgG4;
complementarity determining region; CDR; monoclonal antibody; MAb;

Jul 8 08:33

US-08-137-117B-26.mg

10

KW framework; light chain; heavy chain; variable domain;
KW monoclonal antibody; acceptor antibody Eu; transgenic animal; ss.
OS Mus sp.
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..420
FT /*tag= b
PN W09412215-A.
PD 09-JUN-1994.
PF 30-NOV-1993; U11612.
PR 01-DEC-1992; US-983946.
PA (PROT-) PROTEIN DESIGN LABS INC.
PI Co MS;
DR WPI; 94-199974/24.
DR P-PSDB; R55554.
PT New humanised antibody specific for L-selectin - with murine CDR
and human framework regions, inhibits binding of neutrophils to
PT endothelial cells and useful for treating or preventing
PT inflammation
PS Disclosure; Fig. 1b; 60pp; English.
CC An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs
CC corresponding to those of mouse MAb DREG-200 and heavy and light
CC chain variable region frameworks of the human acceptor antibody Eu.
CC Nucleotide and aa sequences are provided for the DREG-200 light
CC (Q66699, R55553) and heavy (Q66700, R55554) chain variable regions
CC and the humanized DREG-200 light (Q66701, R55555) and heavy (Q66702,
CC R55556) chain variable regions. The humanized antibodies can be
CC produced economically in large quantities by expression in mammalian
CC cell culture or in transgenic animals.
SQ Sequence 420 BP; 101 A; 98 C; 115 G; 106 T;

Query Match 66.4%; Score 269; DB 11; Length 420;
Best Local Similarity 87.9%; Pred. No. 1.26e-151;
Matches 312; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Db 1 atggaatggagttgatatattcttctctcctgtcagaaactgcagggtgtccactctgag 60
|||||
Qy 1 ATGGGATGAGCGGGATCTTCTCTCTCTCTGTCAGGAACTGCGAGGTGCCACTCTGAG 60
|||||
Db 61 gtccagctgcagcagctgtggacctgacctggtaaagcctggggcttcagtgaaagtctcc 120
|||||
Qy 61 ATCCAGCTGCACAGCTGTGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120
|||||
Db 121 tgcagggtcttgatcacattcactagctatgtatgcactgggtgaagcagagcct 180
|||||
Qy 121 TGCAGGCTTCTGGTTACTCATTCACTAGCTATTACATACACTGGGTGAGCAGAGCCAT 180
|||||
Db 181 gggcagggttcgtgagtgatgatatattatctctcaaatgatggtactaagtaaat 240
|||||
Qy 181 GGAAGAGCCTTGAGTGGATTTGGATATTGATCTCTTCAATGGTGGTACTAGCTACAAC 240
|||||
Db 241 gagaagttcaaaagcagggccacactgactctcaacaaatcctccagcagcctacatg 300
|||||
Qy 241 CAGAAATTCAGGGCAAGGCCACATTGACTGTTGACAAATCTTCCAGCAGCCTCATG 300
|||||
Db 301 gagctcagcagcttgacctctgaggactctcggtctattactgtgcaagggagg 355
|||||
Qy 301 CATCTCAGAGCGCTGCATCTGAGGACTCTGCAGTCTATTACTGTGCAAGGGGGG 355
|||||

RESULT 8
ID Q08607 standard; DNA; 471 BP.
AC Q08607;

DT 04-MAR-1993 (first entry)
DE Co-1 Heavy Chain V Region (mouse).
KW Monoclonal antibody; chimera; light; heavy; chain; constant;
KW variable; antigen; diagnosis; cancer; tumour; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 52..471
FT /*tag= a
PN W09007569-A.
PD 22-MAR-1990.
PF 06-SEP-1989; U03852.
PR 06-SEP-1988; US-240624.
PR 08-SEP-1988; US-241744.
PR 13-SEP-1988; US-243739.
PR 04-OCT-1988; US-253002.
PR 19-JUN-1989; US-367641.
PR 21-JUL-1989; US-382768.
PA (ITGE-) INT GENETIC ENG INC.
PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
DR WPI; 90-115825/15.
DR P-PSDB; R09425.
PT Chimeric mouse-human antibodies - prepd. using genes coding for
PT constant human region murine variable region, esp. to 3 tumour
PT antigen
PS Clam 13; Page 123 + Fig 22; 173pp; English.
CC Shown is the nucleotide sequence from the end of the oligo-dC tail
CC to the JH4-Ch1 junction. The sequence is used in the prodn. of a
CC chimeric antibody mol. comprising two light chains and two heavy chains,
CC each having a constant region (human) and a variable region (murine)
CC having specificity to an antigen bound by murine monoclonal antibody
CC (MAb) Co-1. The chimeric antibodies can be used for any purpose for
CC which the original murine MAb can be used, with the advantage that
CC they are more compatible with the human body. They are esp. used for
CC the diagnosis and treatment of cancer.
SQ Sequence 471 BP; 115 A; 120 C; 115 G; 121 T;
Query Match 66.2%; Score 268; DB 5; Length 471;
Best Local Similarity 87.9%; Pred. No. 5.56e-151;
Matches 311; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Db 52 atggaatgagttgattcttctctctctgtcaggaactgcaggtgtccactctgag 111
Qy 1 ATGGGATGGAGGGGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAG 60
Db 112 gtccagctgcagcagctctgcagctgagctgtgtaagcctgggggttcagtgagatgcc 171
Qy 61 ATCCAGCTGCAGCAGCTCTGCACCTGAGCTGATGAGAGCTGGGGCTTCAGTGAAGATATCC 120
Db 172 tgcagagctcttgatcacacattactagctatgttatgcaactgggtgaagcagaagcct 231
Qy 121 TCGAAGGCTTCTGGTTACTCTATCTACTAGCTATTACATACATCTGGGTGAGCAGAGCCAT 180
Db 232 ggcgcaggcccttgagtgattgatatatttaattccttacaatgaggttactagttacaat 291
Qy 181 GGAAGAAGAGCTTGAATGGATATATTTGATCTCTTCAATGGGTGGTACTAGCTACAAAC 240
Db 292 ggcgcctcaaggcagggccacactgacttcagacaatcctccagcagcagctacatg 351
Qy 241 CAGAAATCAAGSGGAAGGCCACATTGACTCTTGCACAAATCTTCCAGCAGCAGCTACATG 300
Db 352 gagctcagcagcagctgacoccttgaggagctctgoggtctattactgtgcaagggag 405
Qy 301 CATCTCAGCAGGCTGACATCTGAGGACTCTGCAGCTCTATTACTGTTCAGGGGGG 354

RESULT 9
ID Q11291 standard; cDNA; 499 BP.
AC Q11291;
DT 14-JUN-1991 (first entry)
DE Encodes murine monoclonal 14.18 H chain V region.
KW chimaeric binding protein; immunoglobulin; variable region; mouse;
KW ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT mat_peptide 98..499
FT /*tag= a
FT sig_peptide 41..97
FT /*tag= b
FT /label= leader
PN W09104329-A.
PD 04-APR-1991.
PF 01-AUG-1990; U04301.
PR 20-SEP-1989; US-409889.
PA (ABBO) ABBOTT LABORATORIES.
PI Gillies SD;
DR WPI; 91-117518/16.
DR P-PSDB; R11597.
PT Fusion protein prodn. - e.g. having dual biological activity,
PT esp. antibodies, by transfecting host cell with constructed
PT cassette and second DNA sequence
PS Example; Fig 2; 52pp; English.
CC Two separate H and L chain cDNA libraries were prepared from mRNA
CC isolated from the murine hybridoma cell line 14.18. The lambda gt10
CC library was enriched for full-length L- and H-chains. It was screened
CC by filter hybridisation using various C region probes. Ten phage
CC clones from each screening were analysed further by restriction
CC analysis. The longest H cDNA sequence was sequenced. It appears to
CC encode a normal length Ig leader peptide. To ensure translation
CC starts from the second ATG codon once additional 5' sequences have
CC been added to the insert, the cDNA is truncated by limited Bal31
CC exonuclease treatment. An XhoI linker was then added to give a
CC sequence which, when expressed, will result in an mRNA encoding a
CC normal Ig leader sequence and a functional variable region.
CC See also Q11292.
SQ Sequence 499 BP; 127 A; 131 C; 119 G; 122 T;
Query Match 65.9%; Score 267; DB 2; Length 499;
Best Local Similarity 87.8%; Pred. No. 2.45e-150;
Matches 310; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Db 41 atggatggaactggatctttatttattcctgtcgttaactacaggtgtccactctgag 100
Qy 1 ATGGGATGGAGGGGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAG 60
Db 101 gtccaactgctgagctctggacctggagctggaggaagcctgagccttcagtcatgatctcc 160
Qy 61 ATCCAGCTGCAGCAGCTCGACCTGCAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120
Db 161 tgcagagctcttggttctctcattcactggctacacatgaactgggtgagcagaacatt 220
Qy 121 TCGAAGGCTTCTGGTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTT 180
Db 221 ggaagagccttgatggattggagctattgatccttactatgggtgaactagctacaac 280
Qy 181 GGAAGAAGGCTTGGATGGATATATTTGATCTCTTTCAATGGGTGGTACTAGCTACAAAC 240
Db 281 cagaagtccaaggcagggccacactgactgtagacaatcgtccagcagcagctacatg 340
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

1111

Db 121 tgcaggctctgttactcattcactggctacaccatgaactgggtgaagcagagccat 18

The sequences given in Q43846-48 represent the expression vectors pAH4625, pAH4807 and pAH4808. These vectors represent the cloning of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4 respectively, with the variable region of the murine monoclonal antibody 128.1. These plasmids each encode a chimeric monoclonal antibody in which the heavy chain (VH) is derived from a murine

RESULT 13
ID Q43848 standard: DNA: 10844 BP.

FT /note= "Murine 128.1 VH/hu

FT /note= "Murine 128.1 VH/human gamma-4 CH1"

```
FT CDS 4999..5034
FT /*tag= c
FT /note= "Undefined ORF1"
FT CDS 5153..5482
FT /*tag= d
FT /note= "Undefined ORF2"
FT CDS 5580..5900
FT /*tag= e
FT /note= "Undefined ORF3"
FT unsure 6128..6329
FT /*tag= f
FT unsure 6336..6635
FT /*tag= g
FN W09310819-A.
PD 10-JUN-1993.
PF 24-NOV-1992; U10206.
PR 26-NOV-1991; US-800458.
PA (ALKE-) ALKERMES INC.
PI Friden PM;
DR P-PSDB; R41715-18.
PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders
PS Disclosure; Fig 19A-F; 151pp; English.
CC The sequences given in Q43846-48 represent the expression vectors
CC pAH4625, pAH4807 and pAH4808. These vectors represent the cloning
CC of the different human gamma isotypes, gamma-2, gamma-3 and gamma-4
CC respectively, with the variable region of the murine monoclonal
CC antibody 128.1. These plasmids each encode a chimeric monoclonal
CC antibody in which the heavy chain (VH) is derived from a murine
CC source and the sequences encoding CH1, CH2 and CH3 are derived from
CC a human source. These vectors in combination with the chimeric light
CC chain vector, pAG4611 (see also Q43845), were transfected into SP2/0
CC cells and clones were isolated. Antibody analysis using biosynthe-
CC tically labelled proteins, immunoprecipitation and SDS-PAGE indicated
CC appropriate bands for the heavy and light chains as well as the
CC assembled antibody for the gamma-3 and gamma-4 chimeras. No detectable
CC protein was isolated for the gamma-2 transfectants. 128.1 is an anti-
CC human transferrin receptor antibody which binds to the transferrin
CC receptor on brain capillary endothelial cells. This antibody may be
CC used in a conjugate in which it is linked to a neuropharmaceutical or
CC diagnostic agent. The conjugate may be used to treat or prevent
CC neurological disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC Parkinsons and Alzheimers disease. It may also be used for diagnostic
CC methods.
SQ Sequence 10844 BP; 2173 A; 2228 C; 2150 G; 2063 T;

Query Match 64.9%; Score 263; DB 7; Length 10844;
Best Local Similarity 87.3%; Pred. No. 9.25e-148;
Matches 308; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Db 3907 atggaatggagctgggaatgctctctcctgtcaggaaactgaggtgtccgctctgag 3966
||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 ATGGGATGGAGCGGGGATTTCTCTCTCTCTGTCTGTCAGGAACATGCAAGGTGTCCACTCTGAG 60

Db 3967 gtccagctcaacagtctgagacctgaactgggtgaagcctggagcttcaatgaagattcc 4026
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 ATCCAGCTGCAGCAGTCTGGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120

Db 4027 tqcaaggtcttctggttactcattcaactgacctgaacctgaactgggtgaagcagagccat 4086
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 TCGAAGGCTTCTGGTTACTTACTTACTAGTATTATACATAGTCTGCTGCAAGGCGCAT 180
```

```
Db 4087 ggagagaaccttgagtgattggacgtattaactcctcacaatgggtggtactgactacaac 4146
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 181 GGAAGAGCCCTTGAGTGGATTGGATATATTGATCTTTCAATGCTGTACTAGCTACAAC 240

Db 4147 cagaagttcaaggaacaggccctttaaactctagacagtgatcaccacacagccctacatg 4206
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 CAGAAATTCAGGCGCAAGCCACATTTGACTCTTTGACAAATCTTCAGCAGCAGCCTACATG 300

Db 4207 gagctcctcagtcgtgacatctgagagcctctgcagctctattactgtgcaagagg 4259
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 CATCTCAGCAGCCTGACATCTGAGGACTCTCGAGTCTATTACTTCTGCAAGGGG 353

RESULT 14
ID Q43844 standard; DNA; 11529 BP.
AC Q43844;
DT 20-OCT-1993 (first entry)
DE Plasmid pAH4602.
KW Polymerase chain reaction; primer; PCR; amplify; murine;
KW heavy/light; chain; variable; constant; region; anti-human;
KW transferrin; receptor; antibody; brain; capillary;
KW endothelial cell; conjugate; neuropharmaceutical;
KW diagnostic; agent; tumour; AIDS; stroke; epilepsy;
KW Parkinsons disease; Alzheimers disease; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT unsure 2070..3769
FT /*tag= a 3907..4611
FT /*tag= b
FT /*tag= c
FT /note= "VH and CH DNA derived by PCR"
FT sig_peptide 3097..3963
FT /*tag= d
FT /note= "Leader sequence"
FT mat_peptide 3964..4611
FT /*tag= d
FT /note= "Mature VH/CH region"
FT CDS 5000..5044
FT /*tag= e
FT /note= "Undefined ORF"
FT CDS 5163..5492
FT /*tag= f
FT /note= "Undefined ORF2"
FT CDS 5589..5909
FT /*tag= g
FT /note= "Undefined ORF2"
FT unsure 6118..7321
FT /*tag= h 8177..8201
FT /*tag= i
FN W09310819-A.
PD 10-JUN-1993.
PF 24-NOV-1992; U10206.
PR 26-NOV-1991; US-800458.
PA (ALKE-) ALKERMES INC.
PI Friden PM;
DR WPI; 93-196742/24.
DR P-PSDB; R41682-85.
PT Antibody conjugates specific for transferrin receptor - used
PT for diagnosis and treatment of cancer, AIDS and neurological
PT disorders
PS Disclosure; Fig 11A-G; 151pp; English.
CC This sequence represents the expression vector pAH4602.
CC This vector contains open reading frames encoding the heavy
```

[illegible]

FT	unsure	11..1710
----	--------	----------

Jul 8 08:37

US-08-137-117B-26.rst

1

WAVES RELEASE (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:44:30 1996; MasPar time 187.70 Seconds

Tabular output not generated. 775.696 Million cell updates/sec

Title: >US-08-137-117B-26

Description: (1-405) from US08137117B.seq

Perfect Score: 405

N.A. Sequence: 1 ATGGGATGGAGCGGATCTT.....CTCTGTCACGTCTCTGCA 405

Comp: TACCTACTCGCCCTAGAA.....GAGCAGTGACAGACGT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 518261 seqs, 179750453 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-STs

1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94
EST-STs-TWO
95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5
100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10
105:gnEST11 106:gnEST12 107:gnEST13 108:gnEST14 109:gnEST15
110:gnEST16 111:gnEST17 112:gnEST18 113:gnEST19 114:gnEST20
115:gnEST21 116:gnEST22 117:gnEST23 118:gnEST24 119:gnEST25
120:gnEST26 121:gnEST27 122:gnEST28 123:gnEST29 124:gnEST30

Database:

95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5
100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST10
105:gnEST11 106:gnEST12 107:gnEST13 108:gnEST14 109:gnEST15
110:gnEST16 111:gnEST17 112:gnEST18 113:gnEST19 114:gnEST20
115:gnEST21 116:gnEST22 117:gnEST23 118:gnEST24 119:gnEST25
120:gnEST26 121:gnEST27 122:gnEST28 123:gnEST29 124:gnEST30

Jul 8 08:37

US-08-137-117B-26.rst

2

128:enEST20 129:enEST21 130:enEST1 131:enEST2 132:enEST3

Statistics: Mean 10.062; Variance 1.818; scale 5.534

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	100	24.7	287	69	T27609	EST101034 Homo sapien	1.46e-157
2	100	24.7	287	127	HS27609	EST101034 Homo sapien	1.46e-157
3	95	23.5	238	122	HS67011	EST89669 Homo sapiens	9.24e-147
4	95	23.5	238	70	T29670	EST89669 Homo sapiens	9.24e-147
c 5	88	21.7	209	125	HS93811	EST61186 Homo sapiens	9.47e-132
c 6	88	21.7	209	70	T28938	EST61186 Homo sapiens	9.47e-132
7	72	17.8	385	58	R86288	Yp12e09.r1 Homo sapie	4.76e-98
8	54	13.3	299	69	T27727	EST13874 Homo sapiens	1.35e-61
9	54	13.3	299	127	HS27727	EST13874 Homo sapiens	1.35e-61
10	51	12.6	330	64	SSCID10	S.scrofa mRNA; expres	9.76e-56
11	51	12.6	330	129	SSCID10	S.scrofa mRNA; expres	9.76e-56
12	43	10.6	169	79	T64512	Yc24f06.r1 Homo sapie	1.53e-40
13	43	10.6	303	57	R83139	Yp11q03.r1 Homo sapie	1.53e-40
14	43	10.6	419	100	H73816	Yellib01.r1 Homo sapie	1.53e-40
15	43	10.6	419	124	HS816226	Yellib01.r1 Homo sapie	1.53e-40
16	42	10.4	297	127	HS27868	EST18962 Homo sapiens	1.08e-38
17	42	10.4	297	69	T27868	EST18962 Homo sapiens	1.08e-38
18	39	9.6	430	123	HS787240	Yj91h09.r1 Homo sapie	3.11e-33
19	39	9.6	430	54	R72787	Yj91h09.r1 Homo sapie	3.11e-33
20	35	8.6	478	123	HS753236	Yp21q01.r1 Homo sapie	3.58e-26
21	35	8.6	478	16	H43753	Yp21q01.r1 Homo sapie	3.58e-26
22	29	7.2	97	17	H44771	Yp20e11.r1 Homo sapie	3.50e-16
23	29	7.2	97	123	HS771238	Yp20e11.r1 Homo sapie	3.50e-16
24	29	7.2	147	16	H42647	Yp13a12.r1 Homo sapie	3.50e-16
25	29	7.2	331	127	HS277715	EST13381 Homo sapiens	3.50e-16
26	29	7.2	331	69	T27715	EST13381 Homo sapiens	3.50e-16
27	28	6.9	228	11	H24604	Y140b06.r1 Homo sapie	1.32e-14
28	27	6.7	169	47	R48619	Yj68a01.r1 Homo sapie	4.68e-13
29	27	6.7	174	70	T29212	EST73046 Homo sapiens	4.68e-13
30	27	6.7	174	116	HS21211	EST73046 Homo sapiens	4.68e-13
31	27	6.7	234	127	HS28164	EST30734 Homo sapiens	4.68e-13
32	27	6.7	234	69	T28164	EST30734 Homo sapiens	4.68e-13
33	27	6.7	325	122	HS71611	EST91759 Homo sapiens	4.68e-13
34	27	6.7	325	70	T29716	EST91759 Homo sapiens	4.68e-13
35	26	6.4	367	78	T60021	Yc01q07.r1 Homo sapie	1.54e-11
36	26	6.4	369	10	H22104	Y134f04.r1 Homo sapie	1.54e-11
37	25	6.2	253	70	T29661	EST89449 Homo sapiens	4.67e-10
38	25	6.2	253	122	HS66110	EST89449 Homo sapiens	4.67e-10
39	25	6.2	309	12	H27953	Y162c09.r1 Homo sapie	4.67e-10
40	25	6.2	362	17	H44273	Yp17c03.r1 Homo sapie	4.67e-10
41	25	6.2	362	117	HS273234	Yp17c03.r1 Homo sapie	4.67e-10
42	25	6.2	434	87	T93178	Ys24e07.r1 Homo sapie	4.67e-10
43	25	6.2	446	53	R71741	Yj85d11.r1 Homo sapie	4.67e-10
44	25	6.2	471	17	H45128	Yp66f01.r1 Homo sapie	4.67e-10
45	25	6.2	471	114	HS128238	Yp66f01.r1 Homo sapie	4.67e-10

ALIGNMENTS

RESULT LOCUS	1	T27609	287 bp	mRNA	EST	06-SEP-1995
--------------	---	--------	--------	------	-----	-------------

Jul 8 08:37

US-08-137-117B-26.rst

3

DEFINITION EST101034 Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJC regions (GB:M18512) (HT:3056).

ACCESSION T27609

KEYWORDS EST.

SOURCE human primer=M13 Reverse library-Human Pancreas.

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonadta; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 287)

REFERENCE

AUTHORS Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.-W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M., Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S., Kelley J.M., Klimex K.M., Kelley J.C., Liu L.-I., Marmaros S.M., Merrick J.M., Moreno-Palauques R.F., McDonald L.A., Nguyen D.T., Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.-J., Dimke D., Feng P., Ferrie A., Fischer C., Hastings G.A., He W.-W., Hu J.-S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H., Meisner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C., Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M. and Venter J.C.

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence

JOURNAL Unpublished (1995)

COMMENT

Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

NCBI gi: 609707

FEATURES Location/Qualifiers

source 1..287

/organism="Homo sapiens"

/note="human"

<1..>287

BASE COUNT 62 a 77 c 85 g 60 t 3 others

ORIGIN

Query Match

Best Local Similarity 24.7%; Score 100; DB 69; Length 287;

Matches 167; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Db 14 atggactggacctggaggtacctctcttctgtggcagcagccanaggagccactccag 73

QY 1 ATGGGATGGAGCGGGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCG 60

Db 74 gtgcacctggtgcactctggggctgaggtgaagaagcctggggcctcagtgaggtctcc 133

QY 61 ATCCAGTCGACGACGCTGAGCTGATGAAGCGCTGGGGCTTCAGTCAGATATCC 120

Db 134 tgcgaagctctggatcgcgcttcacogactactatatacactgattcgcagggccct 193

Jul 8 08:37

US-08-137-117B-26.rst

4

QY 121 TCCAAGCCTCTGCTTACTCATTCTACTAGTATTACATACACTGGTGAAGCAGGCAT 180

Db 194 ggacaaggcttgatggatggatggatgaacctcgcagtcggtgcccaact 248

QY 181 GGAAGAGCCTTGAGTGGATATATTGATCTTCAATGCTGCTACTAGCT 235

RESULT 2

ID HST27609 standard; RNA; EST; 287 BP.

AC T27609;

DT 12-JAN-1995 (Rel. 42, Created)

DE 07-SEP-1995 (Rel. 45, Last updated, Version 3)

DE EST101034 Homo sapiens cDNA 5' end similar to immunoglobulin mu

DE heavy chain, VDJC regions (GB:M18512) (HT:3056).

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

RN [1]

RP 1-287

RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,

RA Bult C.J., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D.,

RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,

RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,

RA Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,

RA Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,

RA Kelley J.M., Klimex K.M., Kelley J.C., Liu L.I., Marmaros S.M.,

RA Merrick J.M., MORENO-PALAUQUES R.F., McDonald L.A., Nguyen D.T.,

RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,

RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,

RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,

RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,

RA Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,

RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,

RA Meisner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,

RA Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,

RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;

*Initial Assessment of Human Gene Diversity and Expression

RT Patterns Based Upon 52 Million Basepairs of cDNA Sequence";

RL Unpublished.

CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper

CC Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:

CC tdbinfo@tdb.tigr.org For clone availability, additional sequence

CC and expression information related to this EST, please contact the

CC TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 609707

FH Key Location/Qualifiers

FT source 1..287

FT /organism="Homo sapiens"

FT /note="human"

FT mRNA <1..>287

SQ Sequence 287 BP; 62 A; 77 C; 85 G; 60 T; 3 other;

Query Match

Best Local Similarity 24.7%; Score 100; DB 127; Length 287;

Matches 167; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Db 14 atggactggacctggaggtacctctcttctgtggcagcagccanaggagccactccag 73

QY 1 ATGGGATGGAGCGGGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCG 60

Db 74 gtgcacctggtgcactctggggctgaggtgaagaagcctggggcctcagtgaggtctcc 133

QY 61 ATCCAGTCGACGACGCTGAGCTGATGAAGCGCTGGGGCTTCAGTCAGATATCC 120

Db 134 tgcgaagctctggatcgcgcttcacogactactatatacactgattcgcagggccct 193

QY 61 ATCCAGCTGCAGCAGCTCTTGACCTGAGCTGATGAAGCCTGGGGCTTCAGTGAAGATATCC 120

Db 134 tgcagaactctgatacgccctcaccgaactactatatactgattgcagagggccct 193

QY 121 TCGAAGGGCTCTGGTTACTATTCTACTAGCTATTACATACATCGGTGAAGCAGAGGCAT 180

Db 194 gcaacagggttgaatgtagtgatggatgaacctcgcagtcgagtgtgccacaact 248

QY 181 GAAAGAGCCTTCAGTGGATTTGATATTTATGCTTTCAATGTGGTACTAGCT 235

RESULT	3	
ID	AD	H567011 standard; RNA; EST; 238 BP.
AC	TT9670;	
DT	09-JAN-1995 (Rel. 42, Created)	
DE	08-SEP-1995 (Rel. 45, Last updated, Version 2)	
DE	EST89669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy	
DE	chain V region (GB:X61012) (HT:3230).	
DE	EST.	
KW	Homo sapiens (human)	
OS	Homo sapiens (human)	
OC	Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;	
OC	Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.	
NC	[1]	
RP	1-238	
RA	Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,	
RA	Bult C.J., Lee N., Kirkness E.F., Weinstein K.G., Gocayne J.D.,	
RA	White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,	
RA	Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,	
RA	Fitzgerald L.M., FitzHugh W.M., Fritchman J.L., Geodhagen N.S.M.,	
RA	Glodok A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,	
RA	Kelley J.M., Klimke K.M., Kelley J.C., Liu L.I., Marmaros S.M.,	
RA	Merrick J.M., MORENO-PALAMQUES R.F., McDonald L.A., Nguyen D.T.,	
RA	Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,	
RA	Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,	
RA	Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,	
RA	Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrie A.,	
RA	Fischer C., Hastings G.A., He W.M., Hu J.S., Greene J.M.,	
RA	Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,	
RA	Weisner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C.,	
RA	Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,	
RA	Haeslein W.A., Fields C., Fraser C.M., Venter J.C.;	
RT	"Initial Assessment of Human Gene Diversity and Expression	
RT	Patterns Based Upon 52 Million Baeepairs of cDNA Sequence";	
RL	Unpublished.	
CC	Contact: Venter, JC The Institute for Genomic Research 932 Clopper	
CC	Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:	
CC	tdbinfo@db.tigr.org For clone availability, additional sequence	
CC	and expression information related to this EST, please contact the	
CC	TIGR Database (tdbinfo@db.tigr.org). NCBI gi: 611768	
CH	Key	Location/Qualifiers
EH		
FT	source	1..238
FT		/organism="Homo sapiens"
FT		/note="human"
FT	mrna	<1..>238
SQ	Sequence 238 BP; 46 A; 70 C; 69 G; 52 T; 1 other;	

```

Query Match      23.5%; Score 95; DB 122; Length 238;
Best local Similarity 74.0%;
Matches 145; Conservative 0; Mismatches 147;
Indels 0; Gaps 0;

Db 43 atggactggacctggagcactcttttttgggtggcagcagcaacaggtggccactccag 102
Qv 1 ATGGGATGAGCGGATCTTTCTCTCTCTGTGCAGAACTGCAGGTGTCACCTCTGAG 60

```

RESULT	4	T29670	238 bp	mRNA	EST	06-SEP-1995
LOCUS		EST89669	Homo sapiens	cDNA 5'	end similar to immunoglobulin heavy chain V region (GB:X61012) (HT:3230).	
DEFINITION						

ACCESSION T29670
KEYWORDS EST.

human primer=M13 Reverse library=human Small intestine.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Hominoidei Homo.

REFERENCE 1 (bases 1 to 238)

AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Ene, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fitchman, J.L., Geoghagan, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S., Kelley, J.M., Klimek-Kaln, K., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.J.B., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 52 Million Basepairs of cDNA Sequence
Unpublished (1995)

Contact: Venter, JC
 The Institute for Genomic Research
 932 Clopper Rd, Gaithersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@tdb.tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please contact the TIGR Database
 (tdbinfo@tdb.tigr.org).

```

NCBI gi: 611768
FEATURES
source          location/Qualifiers
                1..238
                /organism="Homo sap
                /note="human"
                mRNA
                <1..>238

```


Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@db.tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please contact the TIGR Database
 (tdbinfo@db.tigr.org).

NCBI gi: 611036 Location/Qualifiers
 source 1..209
 /organism="Homo sapiens"
 /note="human"
 mRNA <1..>209
 BASE COUNT 43 a 62 c 48 g 55 t 1 others
 ORIGIN

Query Match 21.7%; Score 88; DB 70; Length 209;
 Best Local Similarity 71.9%; Pred. No. 9.47e-132;
 Matches 143; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Db 3 gatgtntccctggttaagtgaactctgacctggaactctgtgaaatattttgtgtaccac 62
 Cp 281 GATTTGTCAACAGTCAATGTCCTTCGCTTCGAATTTTGGTGTGCTAGCTAGTACCACCA 222

Db 63 ttgccagctgtgatccatccatccatcaagccttctgcgggggacctggcgaccacaa 122
 Cp 221 TTGAAGAGTCAATATATCAATCACTCAAGGCTCTTCCATGCGCTCTGCTTCACCCAG 162

Db 123 tgcatagcatagctagctgaaggtgtatccagaagccttcaggaaacottcaactgagcc 182
 Cp 161 TGTATGTATAGTACTAGTGAATGAGTACAGAGCGCTTGCAGGATATCTTCACTGAAGCC 102

Db 183 ccaggcttctcacctcag 201
 Cp 101 CCAGGCTTCATCAGCTCAG 83

RESULT 7
 LOCUS yp12a09.r1 Homo sapiens cDNA clone 187240 5' similar to gb:102325
 DEFINITION IG HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);.
 ACCESSION R86288
 KEYWORDS EST.
 SOURCE human clone=187240 library=Soares breast 3NbHBst vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Adult human. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTCAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 385)

REFERENCE
 AUTHORS Hillier, L., Clark, M., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 323
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 944694 Location/Qualifiers
 source 1..385
 /organism="Homo sapiens"
 /clone="187240"
 /note="human"
 BASE COUNT 85 a 104 c 112 g 78 t 6 others
 ORIGIN

Query Match 17.8%; Score 72; DB 58; Length 385;
 Best Local Similarity 70.5%; Pred. No. 4.76e-98;
 Matches 129; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

Db 67 tctgtctgtggttagtccaggtgtcctcactccaggtgcaggtngtcagctctgggg 126
 Yy 23 TCTTCTTCTGTGAGGAAGTGCAGGTCTCCACTCTGAGATCCAGCTGCAGCAGTCTGGAC 82

Db 127 ctgaggtgaagatgcctggggcctcagtgaaagcttctcgaagcagctggttcgcgc 186
 Yy 83 CTGAGCTGATGAGCCTGGGCTTCAGTCAAGATATCTGCAAGGCTTCTGGTTACTCAT 142

Db 187 tcagccaccactacatgcactgggtgcagagccctgggacaaggagatnagtgcctg 246
 Yy 143 TCACCTAGCTATTACATACACTGGGTGAGCAGACCATGGAAGAGCC-TTGAGTGGATT 201

Db 247 gga 249
 Yy 202 GGA 204

RESULT 8
 LOCUS T27727 299 bp mRNA EST 06-SEP-1995
 DEFINITION EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu (gamma) heavy chain, V(IV)DJC regions (HT:3057).
 ACCESSION T27727
 KEYWORDS EST.
 SOURCE human primer=M13 Reverse library=Human Testis.

ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 299)

REFERENCE
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geodhagen, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle Jr, P.S.,

Kelley, J.M., Klinek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanco, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrrie, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence

JOURNAL Unpublished (1995)

COMMENT

Contact: Venter, JC

The Institute for Genomic Research

932 Clopper Rd, Gaithersburg, MD 20878

Tel: 3018699056

Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression

information related to this EST, please contact the TIGR Database

(tdbinfo@tdb.tigr.org).

NCBI gi: 609825

FEATURES Location/Qualifiers

source

1..299

/organism="Homo sapiens"

/note="human"

mRNA

<1..>299

BASE COUNT 61 a 84 c 82 g 68 t 4 others

ORIGIN

Query Match 13.3%; Score 54; DB 69; Length 299;

Best Local Similarity 63.8%; Pred. No. 1.35e-61;

Matches 125; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Db 35 ggtttcttctctctggtgcagctcccagatgggtctgtcccaggtgcagtgcaag 94

||||| || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||

Qy 14 GGATCTTTCTCTCTCTCTCAGGAACCTGCAGGTGCCACTCTGAGATCCAGCTGCAGC 73

||||| || || || || || || || || || || || || || || || || || || || ||

Db 95 agtcggccaggactggtgaagccttcggagaccctgtccctcacctgcactgtctctg 154

||||| || || || || || || || || || || || || || || || || || || || ||

Qy 74 AGCTGGACCTGAGCTGATGAGCCTGGGCTTCAGTGAAGATATCTTGCAGGCTTCTG 133

||||| || || || || || || || || || || || || || || || || || || || ||

Db 155 qtggctccatcagtagttactactagctggatcgagcagcccccagggaaggaactgc 214

||||| || || || || || || || || || || || || || || || || || || || ||

Qy 134 GTTACTATTCTAGCTAGCTATTACATACACTGGGTGAAGCAGCCATGGAAGACCTTG 193

||||| || || || || || || || || || || || || || || || || || || || ||

Db 215 agtgattgggttatat 230

||||| || || || || || || || || || || || || || || || || || || || ||

Qy 194 AGTGGATTGGATATAT 209

RESULT 9

ID HST27727 standard; RNA; EST; 299 BP.

AC T27727;

DT 12-JAN-1995 (Rel. 42, Created)

DT 07-SEP-1995 (Rel. 45, Last updated, Version 2)

DE EST13874 Homo sapiens cDNA 5' end similar to immunoglobulin mu

DE (gamma) heavy chain, V(IV)DJC regions (HT:3057).

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Primates; Haplothinii; Catarrhini; Homnidae.
RN [1]
RP 1-299
RA Adams M.D., Kerlavage A.R., Fleischmann R.D., Fuldner R.A.,
RA Bult C.J., Lee N., Kirkness E.F., Weinstein K.G., Gocayne J.D.,
RA White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W.,
RA Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D.,
RA FitzGerald L.M., FitzHugh W.M., Fritchman J.L., Geoghagen N.S.M.,
RA Glodek A., Gnehm C.L., Hanna M.C., Hedblom E., Hinkle Jr P.S.,
RA Kelley J.M., Klinek K.M., Kelley J.C., Liu L.I., Marmaros S.M.,
RA Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T.,
RA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L.,
RA Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R.,
RA Weidman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A.,
RA Coleman T.A., Collins E.J., Dimke D., Feng P., Ferrrie A.,
RA Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M.,
RA Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li H.,
RA Meissner P.S., Olsen H., Raymond L., Wei Y.-F., Wing J., Xu C.,
RA Yu G.-L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A.,
RA Haseltine W.A., Fields C., Fraser C.M., Venter J.C.;
RA "Initial Assessment of Human Gene Diversity and Expression
RT Patterns Based Upon 52 Million Basepairs of cDNA Sequence";
RL Unpublished.

CC Contact: Venter, JC The Institute for Genomic Research 932 Clopper

CC Rd, Gaithersburg, MD 20878 Tel: 3018699056 Fax: 3018699423 Email:

CC tdbinfo@tdb.tigr.org For clone availability, additional sequence

CC and expression information related to this EST, please contact the

CC TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: 609825

FH Key Location/Qualifiers

EH source 1..299

FT /organism="Homo sapiens"

FT /note="human"

FT mRNA <1..>299

SQ Sequence 299 BP; 61 A; 84 C; 82 G; 68 T; 4 other;

Query Match 13.3%; Score 54; DB 127; Length 299;

Best Local Similarity 63.8%; Pred. No. 1.35e-61;

Matches 125; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Db 35 ggtttcttctctctggtgcagctcccagatgggtctgtcccaggtgcagtgcaag 94

||||| || || || || || || || || || || || || || || || || || || || ||

Qy 14 GGATCTTTCTCTCTCTCTCAGGAACCTGCAGGTGCCACTCTGAGATCCAGCTGCAGC 73

||||| || || || || || || || || || || || || || || || || || || || ||

Db 95 agtcggccaggactggtgaagccttcggagaccctgtccctcacctgcactgtctctg 154

||||| || || || || || || || || || || || || || || || || || || || ||

Qy 74 AGCTGGACCTGAGCTGATGAGCCTGGGCTTCAGTGAAGATATCTTGCAGGCTTCTG 133

||||| || || || || || || || || || || || || || || || || || || || ||

Db 155 qtggctccatcagtagttactactagctggatcgagcagcccccagggaaggaactgc 214

||||| || || || || || || || || || || || || || || || || || || || ||

Qy 134 GTTACTATTCTAGCTAGCTATTACATACACTGGGTGAAGCAGCCATGGAAGACCTTG 193

||||| || || || || || || || || || || || || || || || || || || || ||

Db 215 agtgattgggttatat 230

||||| || || || || || || || || || || || || || || || || || || || ||

Qy 194 AGTGGATTGGATATAT 209

||||| || || || || || || || || || || || || || || || || || || || ||

RESULT 10

LOCUS SSCID10 330 bp RNA EST 30-AUG-1995

DEFINITION S.scrofa mRNA; expressed sequence tag (5'; clone cld10).

ACCESSION F14516

KEYWORDS diversity region; EST; expressed sequence tag; immunoglobulin;

immunoglobulin heavy chain; joining region; variable region.

OC	Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
ON	Theria; Eutheria; Artiodactyla; Suiformes; Suidae.
RC	[1]
RP	1-330
RT	Winteroe A.K., Fredholm M., Davies W.;
RA	"Evaluation and characterization of a porcine small intestine cDNA
RT	library";
RL	Unpublished.

RP 1-330
RA Winteroe A.K.;
RT ;
RL Submitted (26-JUL-1995) to the EMBL/GenBank/DBJ databases.
RL Winteroe A.K., The Royal Veterinary and Agricultural University,
RL Department of Animal Science and Animal Health, Division of Animal
RL Genetics, Bulowvej 13, 1870 Frederiksberg C, DENMARK
FH Key Location/Qualifiers

FH	source	
FT	1..330	
FT	/organism="Sus scrofa"	
FT	/tissue_type="small intestine"	
FT	/clone_lib="directionally cloned cDNA in XLI-blue MRF"	
FT	/clone="cld10"	
FT	V_region	
FT	1..2330	
FT	/partial	
FT	/product="Ig heavy chain variable VDJ region"	
FT	/note="expressed sequence tag"	
FT	Sequence 330 BP; 71 A; 77 C; 104 G; 76 T; 2 other;	
SQ		

Best Local Similarity 58.7%; Pred. No. 9,76e-56;
Matches 166; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy	45	AGGTGTCCACTCTCAGATCCAGCTGCAGCAGTCTGGACCTTGAGCTTGATGAAGCCTGGGGC	104
Db	105	gtctctgaagactctctgtgtgcgctctggattcaactctgaatggctactacaataaactg	164
Qy	105	TTCAGTGAAGATATCCTGCAGGCTTCTGGTTACTCATTCCACTAGCTATTACATACACTG	164
Db	165	gggtccgcaggctccagggaaggggctggaagtggctggcgctattagtaactagtcgtg	224
Qy	165	GGTCAGCAGAGCCATGGAAAGCCCTTCAGTGGATTGGATATTGATCCTTTCAATGG	224
Db	225	Tagtactactacacagactctgtggaggcgcatccaccatctccaaagacaactccca	284
Qy	225	TGGTACTTACTACCAACCAGAATTCAAGGCGAAGCCACATTGACTGTTGACAAATCTTC	284
Db	285	gaagacgcctatctgcaaatnaacgcctgagacaagaagac	327
Qy	285	CAGCAGACCTACATGCATCTTCAGCAGCCTGCATCTGAGGAC	327

RESULT	12
LOCUS	T64512
DEFINITION	yc24f06.r1 Homo sapiens cDNA clone 81635 5' similar to gb:M18512 IG EST 20-FEB-1995
ACCESSION	T64512
KEYWORDS	HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);
SOURCE	EST.
	human clone=81635 library=Stratagene lung (#937210)
	vector=pBluescript SK+ host=SOLR cells (kanamycin resistant)
	primer=M13RP1 Reitel-EcoRI Rsite2-XhoI Normal lung tissue from a 72 year old male. Cloned unidirectionally. Primer: Oligo dT. Average

host-DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5']
AACTGGAGAAATTAATTAAAGATCTTTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 419)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 261

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

NCBI gi: 1046750

FEATURES

source

Location/Qualifiers

1..419

/organism="Homo sapiens"

/clone="214441"

/note="human"

<1..>419

BASE COUNT

91 a 100 c 116 g 102 t 10 others

ORIGIN

Query Match 10.6%; Score 43; DB 100; Length 419;
Best Local Similarity 58.6%; Pred. No. 1.53e-40;
Matches 146; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Db 27 ctggggggccctgagactctctgtgcagcgtctggattccacttcagtagctatggca 86

||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 98 CTGGGGGCTTCACTGAAGATATCTCGAAGGCTTCTGGTTACTCATTCAGTACGTATTACA 157

Db 87 tgcactgggtccgcaggctccaggcaagggtgagctgggtggcatttatacggtag 146

||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 158 TACACTGGGTGAAGCAGGCGATCGAAGAGCGCTTGATGGATTGGATATATTGATCCTT 217

Db 147 atggaagtaataatactatgcagactcctgcaggcccggtgagcctgattccaccatctccagagaca 206

||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 218 TCAATGCTGCTACTAGCTACACCAAGAAATTCAGGCCAAGGCCCACTTGCATGCTTGACA 277

Db 207 attccaagaacacgctgtatctgcaaatgaacagcctgagagctgaggaacacggtgtgt 266

||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 278 AATCTTCCACACACGCTACATGCATCTCAGCAGCGCTGCATCTGAGCACTCTGCAGTCT 337

Db 267 attactgtg 275

|||||||

Qy 338 ATTACTGTG 346

RESULT

15

ID HS816226 standard; RNA; EST; 419 BP.

AC H73816;

DT 03-NOV-1995 (Rel. 45, Created)

DT 03-NOV-1995 (Rel. 45, Last updated, Version 1)

DE y811b01.r1 Homo sapiens cDNA clone 214441 5' similar to gb:M62726

DE IG HEAVY CHAIN V-III REGION (HUMAN);

KW EST.

OS Homo sapiens (human)

OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;

OC Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

RN [1]

RP 1-419

RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,

RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,

RA Trevasakis E., Waterston R., Williamson A., Wohlmann P., Wilson R.;

RT "The WashU-Merck EST Project";

RL Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC est@watson.wustl.edu High quality sequence stops: 261 Source: IMAGE

CC Consortium, LNL This clone is available royalty-free through LNL

CC ; contact the IMAGE Consortium (info@image.lnl.gov) for further

CC information. NCBI gi: 1046750

FH Key

FH Location/Qualifiers

FH source

1..419

/organism="Homo sapiens"

/clone="214441"

/note="human"

FT mRNA

<1..>419

SQ Sequence 419 BP; 91 A; 100 C; 116 G; 102 T; 10 other;

Query Match 10.6%; Score 43; DB 124; Length 419;

Best Local Similarity 58.6%; Pred. No. 1.53e-40;

Matches 146; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Db 27 ctggggggccctgagactctctgtgcagcgtctggattccacttcagtagctatggca 86

||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 98 CTGGGGGCTTCACTGAAGATATCTCGAAGGCTTCTGGTTACTCATTCAGTACGTATTACA 157

Db 87 tgcactgggtccgcaggctccaggcaagggtgagctgggtggcatttatacggtag 146

||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 158 TACACTGGGTGAAGCAGGCGATCGAAGAGCGCTTGATGGATTGGATATATTGATCCTT 217

Db 147 atggaagtaataatactatgcagactcctgcaggcccggtgagcctgattccaccatctccagagaca 206

||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 218 TCAATGCTGCTACTAGCTACACCAAGAAATTCAGGCCAAGGCCCACTTGTGTGACA 277

Db 207 attccaagaacacgctgtatctgcaaatgaacagcctgagagctgaggaacacggtgtgt 266

||||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 278 AATCTTCCACACACGCTACATGCATCTCAGCAGCGCTGCATCTGAGCACTCTGCAGTCT 337

Db 267 attactgtg 275

|||||||

Qy 338 ATTACTGTG 346

Jul 8 08:37

US-08-137-117B-26.rst

19

Search completed: Mon Jul 8 08:47:49 1996
Job time : 199 secs.

Jul 8 08:20

US-08-137-117B-27.rpt

5

```

Qy 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSLTSDESAVYCARCGN 120
Db 121 yeyvamydgqgtsvrvss 139
      : | | | | | | | | |
Qy 121 -RF-A--YWGQGLTVTVA 135

RESULT 5
ENTRY S21810 #type complete
TITLE Ig heavy chain V region - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
12-Apr-1995
ACCESSIONS S21810
REFERENCE S21810
#authors Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.
#submission submitted to the EMBL Data Library, January 1991
#description Nucleotide sequence of a rearranged VDJ-region of a mouse Ig
mu heavy chain gene and its upstream region.
#accession S21810
##status preliminary
##molecule_type DNA
##residues 1-138 ##label OST
##cross-references EMBL:X56936
GENETICS 15/3
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 138 #molecular-weight 15258 #checksum 1535

Query Match 77.8%; Score 769; DB 5; Length 138;
Best Local Similarity 78.3%; Pred. No. 1.42e-83;
Matches 108; Conservative 11; Mismatches 16; Indels 3; Gaps 2;

Db 1 mgwswifllslgtagvhseqlqsgpelvkgasvriksckasygtftgyihwvkqrp 60
||| ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 MCWSGIFLLSGTAGVHSEIQLOQSGPELMKPGASVKISCKASGYSTSYIHWVKQSH 60

Db 61 ggglewlgwlypgnvmtnkynefkfkatltadksastaymqlesltsedsavycarny 120
: : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSLTSDESAVYCAR-G 119

Db 121 seyglaywgggtltvtva 138
: : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 120 NRF--AYWQGLTVTVA 135

```

```

RESULT 6
ENTRY HVMS8A #type complete
TITLE Ig heavy chain precursor V region (108A) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change
23-Mar-1995
ACCESSIONS A02041
REFERENCE A02041
#authors Givol, D.; Zakut, R.; Effron, K.; Rechavi, G.; Ram, D.; Cohen, J.B.
#journal Nature (1981) 292:426-430
#title Diversity of germ-line immunoglobulin V-H genes.
#cross-references MUID:81245215
#accession A02041
##molecule_type DNA
##residues 1-117 ##label GTV
#note the sequence was determined from the germline gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

```

Jul 8 08:20

US-08-137-117B-27.rpt

6

```

FEATURE
1-19 #domain signal sequence #status predicted #label SIG
20-117 #product Ig heavy chain V region (108A) #status
predicted #label MAT
34-117 #domain immunoglobulin homology #label IMM
SUMMARY #length 117 #molecular-weight 12971 #checksum 8923

Query Match 77.0%; Score 762; DB 2; Length 117;
Best Local Similarity 88.9%; Pred. No. 1.23e-82;
Matches 104; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Db 1 mgwswifllslgtagvhseqlqsgpelvkgasvriksckasygtftdymhbwkqsh 60
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 MCWSGIFLLSGTAGVHSEIQLOQSGPELMKPGASVKISCKASGYSTSYIHWVKQSH 60

Db 61 gkslewigyipynggtgynqkfkskatltvdnssstaymeelsltsedsavyyar 117
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSLTSDESAVYCAR 117

RESULT 7
ENTRY PH0105 #type fragment
TITLE anti-digoxin transfectora antibody light chain V region
precursor - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 21-Nov-1993 #sequence_revision 21-Nov-1993 #text_change
21-Nov-1993
ACCESSIONS PH0105
REFERENCE PH0105
#authors Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.; Haber, E.; Jacobson, M.A.
#journal Mol. Immunol. (1990) 27:901-909
#title Heavy and light chain contributions to antigen binding in an
anti-digoxin chain recombinant antibody produced by
transfection of cloned anti-digoxin antibody genes.
#cross-references MUID:91015092
#accession PH0105
##status preliminary
##residues 1-138 ##label NEA
SUMMARY #length 138 #checksum 3011

```

```

Query Match 76.9%; Score 761; DB 13; Length 138;
Best Local Similarity 76.1%; Pred. No. 1.67e-82;
Matches 105; Conservative 18; Mismatches 12; Indels 3; Gaps 2;

Db 1 mgwswifllslgtagvhseqlqsgpelvkgasvriksckasygtftdymhbwkqsh 60
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 MCWSGIFLLSGTAGVHSEIQLOQSGPELMKPGASVKISCKASGYSTSYIHWVKQSH 60

Db 61 gksldvlgvispsgvtgynqkfkgkatltvdksstaymelrsltsedsavycagsg 120
||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||: ||||:
Qy 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSLTSDESAVYCA-RGG 119

Db 121 nkwardywhgbsvrvss 138
|: | ||||: ||||:
Qy 120 NRFA--YWGQGLTVTVA 135

RESULT 8
ENTRY A30577 #type fragment
TITLE Ig heavy chain precursor V region (MRL10) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 04-May-1989 #sequence_revision 04-May-1989 #text_change
12-Apr-1995

```

Jul 8 08:20

US-08-137-117B-27.rpt

7

```
ACCESSIONS A30577
REFERENCE A30577
#authors Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theofilopoulos, A.N.
#journal J. Exp. Med. (1985) 161:805-815
#title Genetic elements used for a murine lupus anti-DNA autoantibody are closely related to those for antibodies to exogenous antigens.
#cross-references MUID:85159423
#accession A30577
##status preliminary
##molecule_type mRNA
##residues 1-135 #label KOF
##cross-references GB:M37621
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 135 #checksum 8166

Query Match 75.2%; Score 744; DB 5; Length 135;
Best Local Similarity 73.3%; Pred. No. 3.13e-80;
Matches 99; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

Db 1 mgwscifllsagtgagvhsqqlqpgaelvkgasvklckasgyftfeywlnwvkqrp 60
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 1 MGWSGIFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSTSYIHWVKQSH 60
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

Db 61 gglewignlpgssstnynefkfkatltvdtssstaymqsltsedavyyccarlv 120
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYCCARGN 120
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

Db 121 gfaywgggtltvtvsa 135
||||| :|||||
Qy 121 RFAYWGGGTLTVTSA 135
||||| :|||||

RESULT 9
ENTRY PN0444 #type fragment
TITLE Ig heavy chain V region precursor - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
ACCESSIONS PN0444
REFERENCE PN0444
#authors Kaluza, B.; Betzl, G.; Shao, H.; Diamantseini, T.; Weidle, U.H.
#journal Gene (1992) 122:321-328
#title A general method for chimerization of monoclonal antibodies by inverse polymerase chain reaction which conserves authentic N-terminal sequences.
#accession PN0444
##molecule_type mRNA
##residues 1-150 #label KAL
##cross-references GB:L02346
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE 1-19 #domain signal sequence #status predicted #label SIG\
20-150 #product Ig heavy chain V region #status predicted
1-19 #label MAT\
20-150 #domain variable region #label VRG
SUMMARY #length 150 #checksum 9720

Query Match 75.1%; Score 743; DB 5; Length 150;
Best Local Similarity 77.5%; Pred. No. 4.25e-80;
Matches 107; Conservative 13; Mismatches 14; Indels 4; Gaps 3;
```

Jul 8 08:20

US-08-137-117B-27.rpt

8

```
Db 1 mewsifillsgtagvlaevqlqpgaelvkgasvklckasgyiftymdmwvkqsh 60
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 1 MGWSGIFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSTSYIHWVKQSH 60
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

Db 61 gkslewigidpnfids-ssynqkfkgkatltvdkssstaymqltsedavyyccarg 119
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 61 GKSLEWIGYIDP-FNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYCCARG 119
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

Db 120 fpygmgywgggtstvtvs 137
||||| :|||||
Qy 120 NRFA--YMQGGTLTVTSA 135
||||| :|||||

RESULT 10
ENTRY JI0076 #type fragment
TITLE Ig heavy chain precursor V region (anti-phenyloxazolone, 18C10) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 12-Apr-1995
ACCESSIONS JI0076
REFERENCE JI0076
#authors Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
#journal Mol. Immunol. (1988) 25:859-865
#title Combinatorial association of V genes: one VH gene codes for three non-cross-reactive monoclonal antibodies each specific for a different antigen (phOxazolone, NP or GAT).
#cross-references MUID:89096973
#accession JI0076
##molecule_type mRNA
##residues 1-141 #label KAA
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE 1-19 #domain signal sequence #label SIG\
20-141 #product Ig heavy chain #status predicted #label MAT\
50-54 #region complementarity-determining 1\
69-85 #region complementarity-determining 2\
123-135 #region J2 segment\
136-141 #region C
SUMMARY #length 141 #checksum 8784

Query Match 74.8%; Score 740; DB 5; Length 141;
Best Local Similarity 73.3%; Pred. No. 1.07e-79;
Matches 99; Conservative 20; Mismatches 16; Indels 0; Gaps 0;

Db 1 mgwscimflaatatgvhsqqlqpgaelvkgasvklckasgyftfeywlnwvkqrp 60
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 1 MGWSGIFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSTSYIHWVKQSH 60
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

Db 61 grglewigrdpsggtkynefkfkatltvdkpsstaymqsltsedavyyccargp 120
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVYCCARGN 120
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

Db 121 agdywgggtltvtvs 135
||||| :|||||
Qy 121 RFAYWGGGTLTVTSA 135
||||| :|||||

RESULT 11
ENTRY PL0011 #type fragment
TITLE Ig heavy chain precursor V region (4C11) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
```

28-Apr-1995
PL0011
#authors Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
#journal Mol. Immunol. (1988) 25:33-40
#title Structural basis of stimulatory anti-idiotypic antibodies.
#cross-references MJD:88142863
#accession PI0011
##molecule_type mRNA
##residues 1-151 ##label CHE
##experimental source cell line 4C11
##COMMENT This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine response.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
1-19 #domain signal sequence #label SIG\

20-136 #product Ig heavy chain V region (4C11) #label MAT\

50-54 #region complementarity-determining 1\

69-85 #region complementarity-determining 2\

118-125 #region complementarity-determining 3\

137-151 #domain constant region #label COR

SUMMARY #length 151 #checksum 2479

Query Match 74.4%; Score 736; DB 5; Length 151;

Best Local Similarity 77.9%; Pred. No. 3.66e-79;

Matches 106; Conservative 9; Mismatches 20; Indels 1; Gaps 1;

Db 1 mgswifilqlgtagvlsavqlqsgpelkpgasvkisckasgyftdytmhvkqsh 60

Qy 1 MCGSGIFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYFTSYIHWVKQSH 60

Db 61 gkalewigfdpnydnfynkfkdktltvdksattaymelksltseadavyycaasyd 120

Qy 61 GKSLEWIGYIDPENGSTYNQKFKGKATLTVDKSSSTAYMHLSLTSEDSAVYYCARGG- 119

Db 121 galdywgqgstvtvs 136

Qy 120 NREAYWGQGLTVTSA 135

RESULT 12

ENTRY S37483 #type complete

TITLE Ig gamma-2a chain - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

ACCESSIONS S37483

REFERENCE S37483

#authors Duncanson, F.F.D.

#submission submitted to the EMBL Data Library, February 1993

#accession S37483

##status preliminary

##molecule_type mRNA

##residues 1-469 ##label DUC

##cross-references EMBL:X70423

SUMMARY #length 469 #molecule-weight 51549 #checksum 7833

Query Match 73.4%; Score 726; DB 11; Length 469;

Best Local Similarity 74.1%; Pred. No. 7.92e-78;

Matches 103; Conservative 15; Mismatches 17; Indels 4; Gaps 2;

Db 1 mgswifilqlgtagvlsavqlqsgpelkpgasvkisckasgyftdytmhvkqsh 60

Qy 1 MCGSGIFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYFTSYIHWVKQSH 60

Db 61 qggklwlgwypasgntkynenfkgtatltvdtsstaymqlesltseadavycarag 120

Qy 61 GKSLEWIGYIDPENGSTYNQKFKGKATLTVDKSSSTAYMHLSLTSEDSAVYYCARG-G 119

Db 121 atatlldywgqgstltvs 139

Qy 120 NR---FAYWGQGLTVTSA 135

RESULT 13

ENTRY S41429 #type complete

TITLE Ig heavy chain V region (anti-anti-TNFAlpha Mab 1G3) - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 03-Mar-1995

ACCESSIONS S41429

REFERENCE S41429

#authors Saseano, M.; Repetto, M.; Casani, G.; Corti, A.

#submission submitted to the EMBL Data Library, January 1994

#description PCR amplification of antibody variable regions with primers that anneal to constant regions.

#accession S41429

##status preliminary

##molecule_type mRNA

##residues 1-138 ##label SAS

##cross-references EMBL:X77230

SUMMARY #length 138 #molecule-weight 15208 #checksum 9990

Query Match 73.1%; Score 723; DB 11; Length 138;

Best Local Similarity 76.8%; Pred. No. 1.99e-77;

Matches 106; Conservative 12; Mismatches 17; Indels 3; Gaps 3;

Db 1 mgswifilqlgtagvlsavqlqsgpelkpgasvkisckasgdfgtndlhvrqsh 60

Qy 1 MCGSGIFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYFTSYIHWVKQSH 60

Db 61 vrslewigrispyngvtynknfkdkatltvdesstaymelhltseadavyyctptt 120

Qy 61 GKSLEWIGYIDPENGSTYNQKFKGKATLTVDKSSSTAYMHLSLTSEDSAVYYCAR-GG 119

Db 121 vdtwfwywgqglvtvsa 138

Qy 120 -N-RFAYWGQGLTVTSA 135

RESULT 14

ENTRY PL0012 #type fragment

TITLE Ig heavy chain precursor V region (F6-3) - mouse (fragment)

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Apr-1995

ACCESSIONS PI0012

REFERENCE PI0011

#authors Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.;

Kohler, H.

#journal Mol. Immunol. (1988) 25:33-40

#title Structural basis of stimulatory anti-idiotypic antibodies.

#cross-references MJD:88142863

#accession PI0012

##molecule_type mRNA

##residues 1-166 ##label CHE

(TM)

Result No.	Query			ID	Description	Pred. No.
	Score	Match	Length			
1	762	77.0	117	HV14_MOUSE	IG HEAVY CHAIN PRECUR	3.00e-144
2	719	72.7	139	HV07_MOUSE	IG HEAVY CHAIN PRECUR	2.40e-134
3	717	72.5	140	HV02_MOUSE	IG HEAVY CHAIN PRECUR	6.93e-134
4	706	71.4	137	HV11_MOUSE	IG HEAVY CHAIN PRECUR	2.34e-131
5	705	71.3	136	HV15_MOUSE	IG HEAVY CHAIN PRECUR	3.96e-131
6	698	70.6	138	HV48_MOUSE	IG HEAVY CHAIN PRECUR	1.60e-129
7	681	68.9	118	HV31_MOUSE	IG HEAVY CHAIN V REGI	1.27e-125
8	677	68.5	117	HV12_MOUSE	IG HEAVY CHAIN V REGI	1.05e-124
9	675	68.3	117	HV13_MOUSE	IG HEAVY CHAIN V REGI	3.01e-124
10	675	68.3	117	HV52_MOUSE	IG HEAVY CHAIN PRECUR	3.01e-124
11	671	67.8	117	HV49_MOUSE	IG HEAVY CHAIN PRECUR	2.48e-123
12	668	67.2	117	HV04_MOUSE	IG HEAVY CHAIN PRECUR	1.21e-122
13	665	67.2	117	HV06_MOUSE	IG HEAVY CHAIN PRECUR	5.87e-122

Jul 8 08:19

US-08-137-117B-27.rsp

3

Qy 1 MCGSIFLELLSGTAGVHSEIQAGSPELMKPGASVKISCKASGYFTSYIHWKQSH 60
 Db 61 qkewlgviypngqgtgynqkfkakatlvdnssstaymelselstedsaavycar 117
 Qy 61 GKSLEWIGYIDFPNGGTSYNQKFKGKATLVDKSSSTAYMHLSSLTSEDSAVYCAR 117

RESULT 2
 ID HV07 MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-NOV-1990 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RM 81234548
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 RA BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -/- THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
 CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
 CC ANTIBODIES).
 DR PIR; A02034; MHMS18.
 DR HSSP; P01810; 1JHL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT CHAIN 1 19
 FT DOMAIN 20 139 IG HEAVY CHAIN V REGION (B1-8 / 186-2).
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DOMAIN 118 124 D SEGMENT.
 FT DOMAIN 125 139 JH2 SEGMENT.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 139 139
 SQ SEQUENCE 139 AA; 15419 MW; 118806 CN;

Query Match 72.7%; Score 719; DB 4; Length 139;
 Best Local Similarity 71.9%; Pred. No. 2.40e-134;
 Matches 100; Conservative 21; Mismatches 14; Indels 4; Gaps 3;
 Db 1 mgwscimflaatqvhsgvqlqpgaeivkpgasvklsckasgyftsyimhwkqrp 60
 Qy 1 MCGSIFLELLSGTAGVHSEIQAGSPELMKPGASVKISCKASGYFTSYIHWKQSH 60
 Db 61 qkewlgviypngqgtgynqkfkakatlvdnssstaymelselstedsaavycar 120
 Qy 61 GKSLEWIGYIDFPNGGTSYNQKFKGKATLVDKSSSTAYMHLSSLTSEDSAVYCAR-G- 118
 Db 121 ygssyfdywgqgtltvs 139
 Qy 119 -GRR-FAYWGQGLTVTSA 135
 RESULT 3
 ID HV02 MOUSE STANDARD; PRT; 140 AA.
 AC P01746;

Jul 8 08:19

US-08-137-117B-27.rsp

4

DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/J;
 RM 82152818
 RA SIMS J., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
 RA CAPRA J.D.;
 RL SCIENCE 216:309-311(1982).
 DR PIR; A02028; HVMSG7.
 DR HSSP; P01789; 6FAB.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYBRIDOMA; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).
 FT NON TER 140 140
 SQ SEQUENCE 140 AA; 15514 MW; 116859 CN;

Query Match 72.5%; Score 717; DB 4; Length 140;
 Best Local Similarity 73.6%; Pred. No. 6.93e-134;
 Matches 103; Conservative 19; Mismatches 13; Indels 5; Gaps 2;
 Db 1 mgwscifllslsgtagvhselqagseivkpgasvklsckasgyftsyimhwkqrp 60
 Qy 1 MCGSIFLELLSGTAGVHSEIQAGSPELMKPGASVKISCKASGYFTSYIHWKQSH 60
 Db 61 qkewlgviypngqgtgynqkfkakatlvdnssstaymelselstedsaavycar 120
 Qy 61 GKSLEWIGYIDFPNGGTSYNQKFKGKATLVDKSSSTAYMHLSSLTSEDSAVYCAR--- 117
 Db 121 ygssyfdywgqgtltvs 140
 Qy 118 -GGR-FAYWGQGLTVTSA 135

RESULT 4
 ID HV11 MOUSE STANDARD; PRT; 137 AA.
 AC P01755;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (S43).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 81234548
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 RA BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -/- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
 CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
 CC ANTIBODIES).
 DR PIR; A02038; G2MS43.
 DR HSSP; P01772; 1EGV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 137 IG HEAVY CHAIN V REGION (S43).
 FT DOMAIN 20 49 FRAMEWORK 1.

```

61 akslewigvistyntsyngkfkgkatmtvdksstvhmelarltseedsanlycaryyg 120
   :||||| | :| | ||||| ||||| : ||||| |||||
61 gkslewtgydpenggtgtsynokefgkalltwokssstymhmlslltseedsavvyrg-g 119

```

Qy 120 --NRFAYWGQGLVTVSA 135

Qy 120 --NRFAYWGQGLVTVSA 135

UC
EUTHERIA; ROVENTIA.

Jul 8 08:19

US-08-137-117B-27.fsp

7

```

RN SEQUENCE.
RM 84182519
RA DILDROP R., BOVENS J., SIEKEVITZ M., BEYREUTHER K., RAJESKY K.;
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR HSSP; P01772; 1FGV.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 85344 CN;

Query Match 68.9%; Score 681; DB 4; Length 118;
Best Local Similarity 81.4%; Pred. No. 1.27e-125;
Matches 96; Conservative 10; Mismatches 10; Indels 2; Gaps 2;

Db 1 evqlqsgpelvkgasvksackasgyftfdymwkvqshgkslewigdnpnngttsy 60
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 EIQLQSGPELMKPGASVKISCKASGYFTSYIHWVKQSHGKSLIEWIGIDPFNGGTSY 79

Db 61 nqkfkgkatltvdksasatymelrsltsedsavvyccargydpfdwgtgtvtvss 118
+|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVVYCARG-G-NRPAYWGQGLTVTUSA 135

RESULT 8
ID HV12 MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (MOPC 104E).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 83075344
RA KERRY M.R., FUHRMAN J.S., SCHILLING J.W., ROGERS J., SIBLEY C.H.,
RA HOOD L.E.;
RL BIOCHEMISTRY 21:5415-5424(1982).
CC -|- THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS
CC ALSO BEEN DETERMINED.
CC -|- THIS PROTEIN BINDS DEXTRAN.
DR HSP; A02039; MHMS4E.
DR HSSP; P01772; 1FGV.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 82832 CN;

Query Match 68.5%; Score 677; DB 4; Length 117;
Best Local Similarity 81.2%; Pred. No. 1.05e-124;
Matches 95; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

Db 1 evqlqsgpelvkgasvksackasgyftfdymwkvqshgkslewigdnpnngttsy 60
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 EIQLQSGPELMKPGASVKISCKASGYFTSYIHWVKQSHGKSLIEWIGIDPFNGGTSY 79

Db 61 nqkfkgkatltvdksasatymelrsltsedsavvyccardydwyfdwaggtvtvss 117
+|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
SQ SEQUENCE 117 AA; 12983 MW; 82832 CN;

```

Jul 8 08:19

US-08-137-117B-27.fsp

8

```

Qy 80 NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVVYCARGNR-FAYWGQGLTVTUSA 135
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
ID HV13 MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (J558).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RM 80078170
RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;
RL NATURE 283:35-40(1980).
CC -|- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN
CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN
CC THE D AND J SEGMENTS.
CC -|- THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR HSSP; P01789; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 82647 CN;

Query Match 68.3%; Score 675; DB 4; Length 117;
Best Local Similarity 81.2%; Pred. No. 3.01e-124;
Matches 95; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

Db 1 evqlqsgpelvkgasvksackasgyftfdymwkvqshgkslewigdnpnngttsy 60
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 20 EIQLQSGPELMKPGASVKISCKASGYFTSYIHWVKQSHGKSLIEWIGIDPFNGGTSY 79

Db 61 nqkfkgkatltvdksasatymelrsltsedsavvyccardydwyfdwaggtvtvss 117
+|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 80 NQKFKGKATLTVDKSSSTAYMHLSSLTSEDSAVVYCARGNR-FAYWGQGLTVTUSA 135
+|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
ID HV52 MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH558 A1/A4).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RM 85099340
RA YANCOPOULOS G.D., ALT F.W.;
RL CELL 40:271-281(1985).
DR EMBL; M13787; MWIGHVA.
DR PIR; A02029; HWSAL.
DR HSSP; P01772; 1FOR.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH558 A1/A4).

```

OS	EUS MUSCULOS (MUSE).
OC	EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; RODENTIA.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6;
RM	8123458
RA	BOTHELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSC
RA	BALTIMORE D.;
RL	CELL 24:625-637(1981).

17

1

Jul 8 08:21

US-08-137-117B-27.rag

5

Qy 1 MGWGIFFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSTSYIHVWKQSH 60
 Db 61 gkslewgiyypnnggtgynqkfekatlvdksstaymelhltseasvyycatagr 120
 Qy 61 GKSLIEWIGYIDPFNGGTSYNQKFKGKATLVDKSSSTAYMHLSSLTSEDSAVYYCARGN 120
 Db 121 yyyawdgqgtlvtvsa 137
 Qy 121 RF-AV-WGQGLTVTVSA 135

RESULT 4

ID R53328 standard; Protein; 139 AA.
 AC R53328;
 DT 17-NOV-1994 (first entry)
 DE KM-796 heavy chain.
 KW Monoclonal antibody; Ab; ganglioside GM2; chimera;
 KW chimeric antibody; expression vector; heavy; light; chain;
 KW hypervariable region; CDR; constant region; hybridoma;
 KW Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Region 50..54
 FT /label= CDR1
 FT /note= "claim 8"
 FT Region 69..85
 FT /label= CDR2
 FT /note= "claim 8"
 FT Region 118..128
 FT /label= CDR3
 FT /note= "claim 8"
 PN A09346181-A.
 PD 17-MAR-1994.
 PF 07-SEP-1993; 046181.
 PR 07-SEP-1992; JP-238452.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
 PI Shitara K;
 DR WPI; 94-126857/16.
 DR N-PSDB; Q45426.
 PT Humanised antibody specific for ganglioside GM2 - used for
 PT producing a cytotoxic effect on cancers such as melanoma,
 PT neuroblastoma and glioma.
 PS Claim 5; Page 104-105; 191pp; English.
 CC Chimeric human Ab expression vectors are constructed by inserting
 CC the Ab heavy and light chain variable region-encoding cDNA
 CC isolated from hybridomas producing a mouse or rat monoclonal Ab
 CC reacting with the ganglioside GM2 respectively into an expression
 CC vector for use in animal cells which contains the human Ab heavy and
 CC light chain constant region-encoding cDNA. The expression vectors
 CC are introduced into animal cells and the transformant thus obtained
 CC is cultured for the prodn. of a chimeric human Ab reacting with the
 CC ganglioside GM2. In contrast to mouse monoclonal Abs, the chimeric
 CC human Abs will not cause anti-mouse Ig Ab prodn. in the patient's
 CC body but show a prolonged blood half-life, with a reduced frequency
 CC of adverse effects, so that it can be expected to be superior
 CC to mouse monoclonal Abs in the efficacy in the treatment of human
 CC cancer, for instance.
 CC Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603
 CC heavy and light chain sequences are given in Q45426-30.
 CC CDR regions for use in chimeric Abs are indicated in the

Jul 8 08:21

US-08-137-117B-27.rag

6

CC Features Table.
 SQ Sequence 139 AA;
 Query Match 79.9%; Score 790; DB 10; Length 139;
 Best Local Similarity 84.2%; Pred. No. 1.23e-60;
 Matches 117; Conservative 6; Mismatches 12; Indels 4; Gaps 2;
 Db 1 mgwewiflllsgtagvhlseqlqqsgpeelvkpgasvkiackasgytftdymdwkqsh 60
 Qy 1 MGWGIFFLLSGTAGVHSEIQQQSGPELMKPGASVKISCKASGYSTSYIHVWKQSH 60
 Db 61 gkslewgiyypnnggtgynqkfekatlvdksstaymelhltseasvyycatygh 120
 Qy 61 GKSLIEWIGYIDPFNGGTSYNQKFKGKATLVDKSSSTAYMHLSSLTSEDSAVYYCAR-G- 118
 Db 121 yyyawdgqgtlvtvsa 139
 Qy 119 --GNRFAYWGQGLTVTVSA 135
 RESULT 5
 ID R29017 standard; Protein; 135 AA.
 AC R29017;
 DT 30-MAR-1993 (first entry)
 DE pUC-RVh-1220d.
 KW Human; antibody; interleukin-6; receptor; IL-6R; CDR; PCR; mouse;
 KW complementarity determining region; monoclonal; hybridoma; PCR;
 KW plasmid; polymerase chain reaction; amplify.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Leader peptide"
 FT Region 20..49
 FT /label= FR1
 FT Region 50..54
 FT /label= CDR1
 FT Region 55..68
 FT /label= FR2
 FT Region 69..85
 FT /label= CDR2
 FT Region 86..117
 FT /label= FR3
 FT Region 118..124
 FT /label= CDR3
 FT Region 125..135
 FT /label= FR4
 PN W09219759-A.
 PD 12-NOV-1992.
 PF 24-APR-1992; J00544.
 PR 25-APR-1991; JP-095476.
 PR 19-FEB-1992; JP-032084.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
 DR WPI; 92-398882/48.
 DR N-PSDB; Q31391.
 PT Reconstituted human antibody to human interleukin-6 receptor -
 PT has low antigenicity and contains mouse V-region complementarity
 PT determining regions
 PS Disclosure; Page 159-60; 207pp; Japanese.
 CC The sequences given in R29016-17 are portions of monoclonal antibodies
 CC which were encoded by plasmids contained within the mouse hybridoma,
 CC AUK12-20. The DNA encoding the complementarity determining regions
 CC (CDR's) was isolated by polymerase chain reaction. These antibodies
 CC recognise human interleukin-6 receptor (IL-6R). The hybridoma cells

Jul 8 08:21

US-08-137-117B-27.rag

11

KW anti-p55 Tac immunoglobulin (Ig) heavy chain; humanised Ig;
 FH Interleukin-2 (IL-2); treatment of T-cell mediated disorders;
 FT Key Location/Qualifiers
 FT Protein 20..135
 FT /label=mature heavy chain
 PN W09007861-A.
 PD 26-JUL-1990.
 PF 28-DEC-1989; U05857.
 PR 28-DEC-1988; US-290975.
 PR 13-FEB-1989; US-310252.
 PA (PROT-) PROTEIN DESIGN LABS.
 PI Queen CL, Seilick HE;
 DR WPI; 90-253800/33.
 DR N-PSDB; Q05600.
 PT Chimeric immunoglobulin(s) blocking IL-2 binding to receptors -
 PT comprising human framework and murine complementary determining
 PT regions, less immunogenic than murine antibodies
 PS Disclosure; p; English.
 CC The sequence was prepared based upon a comparison of human antibody
 CC EU and human anti-Tac Ab. It is the same as the EU sequence except
 CC at certain defined regions. These are CDRs (amino acids 31-35,
 CC 50-66 and 99-106), positions at which the Anti-Tac amino acid was
 CC more typical of heavy chains than the EU residue (posn.s 27, 93,
 CC 95, 98, 107-109, 111), posn.s immediately adjacent to a CDR of
 CC anti-Tac (posn.s 30 and 67) and where the amino acid was thought to
 CC have close proximity to the antigen-binding site (posn.s 48-68).
 CC Humanised Ig's can bind to IL-2 receptors. They are not significantly
 CC immunogenic in humans, are easily and economically produced and
 CC have a longer half-life in vivo than murine antibodies. They are
 CC useful, optionally attached to a cytotoxic agent, for treatment of
 CC T-cell mediated disorders such as graft or transplant rejection.
 CC See also Q05601.
 SQ Sequence 135 AA;

Query Match 76.7%; Score 759; DB 2; Length 135;
 Best Local Similarity 74.1%; Pred. No. 8.38e-58;
 Matches 100; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
 Db 1 mgswifillegtagvhsqvlvsgaevkpgasvkscksgyftfysrmhwrqap 60
 QY 1 MCGSGIFLLSGTAGVHSEIQQSGPELMKPGASVKISCKASGYSTSYIHWKQSH 60
 Db 61 gqglewlgynpstgyteynqkfkdkatitadestntaymelslrseidavycarggg 120
 QY 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSDSAVYTCARGN 120
 Db 121 vfyvggqgtlvts 135
 QY 121 RFAYMGQGLTVTWSA 135

RESULT 11
 ID R12234 standard; Protein; 140 AA.
 AC R12234;
 DT 19-AUG-1991 (first entry)
 DE Mouse Mab 2G12 H chain V region.
 KW HIV-1; chimera.
 OS Mus ep.
 PN W09107494-A.
 PD 30-MAY-1991.
 PF 13-NOV-1990; U06627.
 PR 13-NOV-1989; US-433703.
 PA (XOMA-) Xoma Corp.
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;

Jul 8 08:21

US-08-137-117B-27.rag

12

DR WPI; 91-178106/24.
 DR N-PSDB; Q12014.
 PT New chimeric mouse human antibodies - used in treatment, diagnosis
 PT and prophylaxis of HIV infections.
 PS Disclosure; Fig 7; 108pp; English.
 CC The mouse VH gene product may be used to produce chimeric mouse-
 CC human Abs against HIV-1 comprising human Ig constant regions and
 CC murine variable regions. These novel sequence are useful in
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be
 CC produced by a bacterial, yeast or mammalian expression system.
 SQ Sequence 140 AA;

Query Match 76.7%; Score 759; DB 2; Length 140;
 Best Local Similarity 80.7%; Pred. No. 8.38e-58;
 Matches 113; Conservative 9; Mismatches 12; Indels 6; Gaps 3;
 Db 1 mgswifillegtagvhsqvlvsgaevkpgasvkscksgyftfeytihwkqsh 60
 QY 1 MCGSGIFLLSGTAGVHSEIQQSGPELMKPGASVKISCKASGYSTSYIHWKQSH 60
 Db 61 gqglewlgynpnnggtytnqkfkdkatliivdksstaymdvrseidavycarrgn 120
 QY 61 GKSLEWIGYIDPFNGGTSYNQKFKGKATLTVDKSSSTAYMHLSSLTSDSAVYTCAR-G- 118
 Db 121 lyyngnfwfaywgqplvtvs 140
 QY 119 ---GN-RFAYMGQGLTVTWS 134

RESULT 12
 ID R08346 standard; protein; 144 AA.
 AC R08346;
 DT 05-MAR-1991 (first entry)
 DE Heavy chain variable region of the BMA-031 Mab.
 KW Human alpha/beta T-cell receptor; TCR; cancer; autoimmune disease.
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Signal peptide
 FT Active-site 50..54
 FT /label= CDR 1 69..85
 FT Active-site
 FT /label= CDR 2 118..128
 FT Active-site
 FT /label= CDR 3
 PN EP-403156-A.
 PD 19-DEC-1990.
 PF 07-JUN-1990; 306178.
 PR 07-JUN-1989; US-362549.
 PR 25-MAY-1990; US-529979.
 PA (GENZ-) GENZYME CORP.
 PA (BEHM) BEHRINGER AG.
 PI Kurrie R, Shearman CW, Moore GP, Seiler F;
 DR WPI; 90-377880/51.
 DR N-PSDB; Q06955, Q06957.
 PT Anti-human alpha-beta T-cell receptor monoclonal antibodies -
 PT used for immunosuppressive therapy in transplantation and in
 PT therapeutic agent for immuno-regulation, e.g. to treat cancer
 PS Disclosure; Table 1A; 44pp; English.
 CC The Mab recognises the epitope on alpha/beta TCR and includes a
 CC mediator response. It is highly effective in clinical application
 CC before, after and during bone marrow transplant surgery, in
 CC treatment of cancer and autoimmune diseases, and has applications in
 CC immunoregulation.

Jul 8 08:22

US-08-137-117B-29.rpr

3

Best Local Similarity 92.9%; Pred. No. 2.52e-89;
Matches 118; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 msaqflgllllcfqgtrcdiqmqttsaslgdrvtiscrasqdiynylnwyqkdp 60
Qy 1 msaqflgllllcfqgtrcdiqmqttsaslgdrvtiscrasqdiynylnwyqkdp 60

Db 61 dgtvkllyvtrhsqgvrfsqsgtdysltisnleqediacyfcqgntlpwtfgg 120
Qy 61 dgtvkllyvtrhsqgvrfsqsgtdysltisnleqediacyfcqgntlpwtfgg 120

Db 121 gtkleik 127
Qy 121 gtkleik 127

RESULT 2
ENTRY A26406 #type complete
TITLE Ig kappa chain V region (Ara-A) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Jun-1989 #sequence_revision 30-Jun-1991 #text_change 12-Apr-1995

ACCESSIONS A26406
REFERENCE A26406
#authors Sanz, I.; Capra, J.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:1085-1089
#title V-K and J-K gene segments of A/J Ars-A antibodies: somatic recombination generates the essential arginine at the junction of the variable and joining regions.

#cross-references MUID:871147197
#accession A26406
#molecule type DNA
#residues 1-128 ##label SAN
#cross-references GB:M15519

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 128 #molecular-weight 14078 #checksum 4901

Query Match 95.5%; Score 868; DB 5; Length 128;
Best Local Similarity 92.9%; Pred. No. 2.43e-88;
Matches 118; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 1 msaqflgllllcfqgtrcdiqmqttsaslgdrvtiscrasqdiynylnwyqkdp 60
Qy 1 msaqflgllllcfqgtrcdiqmqttsaslgdrvtiscrasqdiynylnwyqkdp 60

Db 61 dgtvkllyvtrhsqgvrfsqsgtdysltisnleqediacyfcqgntlpwtfgg 120
Qy 61 dgtvkllyvtrhsqgvrfsqsgtdysltisnleqediacyfcqgntlpwtfgg 120

Db 121 gtkleik 127
Qy 121 gtkleik 127

RESULT 3
ENTRY A34904 #type complete
TITLE Ig kappa chain precursor V region (5-27) - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 12-Apr-1995

ACCESSIONS A34904
REFERENCE A34903
#authors Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
#journal J. Biol. Chem. (1990) 265:133-138

Jul 8 08:22

US-08-137-117B-29.rpr

4

#title Active site structure and antigen binding properties of idiotypically cross-reactive anti-fluorescein monoclonal antibodies.
#cross-references MUID:90094387
#accession A34904
#status preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues 1-126 ##label BED
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 126 #molecular-weight 13839 #checksum 3586

Query Match 94.8%; Score 862; DB 5; Length 126;
Best Local Similarity 93.7%; Pred. No. 1.33e-87;
Matches 118; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 1 msaqflgllllcfqgtrcdiqmqttsaslgdrvtiscrasqdiynylnwyqkdp 60
Qy 2 VSSAQFLGILLLLCFQGTCDIQMTQTTSLSASLGDRVTISCRASQDISSYLNWYQKDP 61

Db 61 gtvkllyvtrhsqgvrfsqsgtdysltisnleqediacyfcqgntlpwtfgg 120
Qy 62 GTIKLLIYVTRHSQGVSRFSGSGTDYSLTINNLEQEDIATYFCQGNLTPYTFGG 121

Db 121 tklein 126
Qy 122 TKLEIN 127

RESULT 4
ENTRY A29380 #type fragment
TITLE Ig kappa chain precursor V region (AC-1001) - mouse (fragment)
ORGANISM #formal name Mus musculus #common name house mouse
DATE 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 12-Apr-1995

ACCESSIONS A29380
REFERENCE A29612
#authors Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.
#journal J. Biol. Chem. (1987) 262:13579-13583
#title Nucleotide and translated amino acid sequences of cDNA coding for the variable regions of the light and heavy chains of mouse hybridoma antibodies to blood group A and B substances.

#cross-references MUID:88007582
#accession A29380
#molecule_type mRNA
#residues 1-122 ##label CHE
##note the authors translated the codon TTC for residue 1 as Leu

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 122 #checksum 9064

Query Match 91.5%; Score 832; DB 5; Length 122;
Best Local Similarity 94.2%; Pred. No. 6.50e-84;
Matches 114; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 1 flgllllcfqgtrcdiqmqttsaslgdrvtiscrasqdiynylnwyqkdpvkl 60
Qy 7 FUGLLLLCFQGTCDIQMTQTTSLSASLGDRVTISCRASQDISSYLNWYQKDPGDIKL 66

Db 61 lhyterlshsqgvrfsqsgtdysltisnleqediacyfcqgntlpwtfggtklei 120
Qy 67 LIYVTRHSQGVSRFSGSGCTDYSLTINNLEQEDIATYFCQGNLTPYTFGGTKLEI 126

Jul 8 08:22

US-08-137-117B-29.rpr

7

```
#accession B28044
##molecule_type mRNA
##residues 1-107 ##label MEE
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 107 #molecular-weight 11738 #checksum 7011

Query Match 78.5%; Score 714; DB 5; Length 107;
Best Local Similarity 94.4%; Pred. No. 1.80e-69;
Matches 101; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 dmqmtqttslaelsgdrvtiscrasqdiynlnwyqkpdgtvkllytserlshgvsps 60
Qy 21 DIQMTQTTSLSASLGRVITISCRASQDISSYLNWYQKPDGTETIKLLIYTSRLSHGVS 80

Db 61 rfsgsgsgtdysltinnleqediatyfcqgntlprtfgggktleik 107
Qy 81 RFSGSGSGTDYSLTINNLEQEDATYFCQGNTLPYTFGGGKLEIN 127
```

```
RESULT 9 KWMSAR #type complete
ENTRY Ig kappa chain V regions (anti-arsonate hybridoma proteins) - mouse
TITLE #formal_name Mus musculus #common_name house mouse
ORGANISM 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change
DATE 05-Apr-1995
```

```
ACCESSIONS A01927
REFERENCE A01927
#authors Siegelman, M.; Capra, J.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1981) 78:7679-7683
#title Complete amino acid sequence of light chain variable regions derived from five monoclonal anti-p-azophenylarsenate antibodies differing with respect to a crossreactive idiotype.
```

```
#cross-references M01D:82150934
#accession A01927
##molecule_type protein
##residues 1-108 ##label SIE
##experimental_source strain A/J
##note having 7-Ser, 92-Tyr, and 93-Met; HP 123E6 differs in having 30-Asn, 92-Lys, and 93-Thr; and HP 91A3 differs in having 8-Pro, 30-Asn, 37-Arg, 84-Ser, and 93-Ala
```

COMMENT The sequence shown is HP R16.7.

```
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE #disulfide bonds #status predicted
23-88 #length 108 #molecular-weight 11910 #checksum 1537
```

```
Query Match 78.5%; Score 714; DB 2; Length 108;
Best Local Similarity 94.4%; Pred. No. 1.80e-69;
Matches 101; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
Db 1 dmqmtqttslaelsgdrvtiscrasqdiynlnwyqkpdgtvkllytserlshgvsps 60
Qy 21 DIQMTQTTSLSASLGRVITISCRASQDISSYLNWYQKPDGTETIKLLIYTSRLSHGVS 80
```

```
Db 61 rfsgsgsgtdysltinnleqediatyfcqgnsprtfgggktleik 107
Qy 81 RFSGSGSGTDYSLTINNLEQEDATYFCQGNTLPYTFGGGKLEIN 127
```

```
RESULT 10 A28044 #type complete
ENTRY
```

Jul 8 08:22

US-08-137-117B-29.rpr

8

```
TITLE Ig kappa chain V region (22B5) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-May-1989 #sequence_revision 19-May-1989 #text_change
12-Apr-1995
ACCESSIONS A28044
REFERENCE A94179
#authors Meek, K.; Sanz, I.; Rathbun, G.; Nisonoff, A.; Capra, J.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:6244-6248
#title Identity of the V-kappa-10-Ars-A gene segments of the A/J and BALB/c strains.
```

```
#cross-references M01D:87317629
#accession A28044
##molecule_type mRNA
##residues 1-107 ##label MEE
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 107 #molecular-weight 11832 #checksum 7241
```

```
Query Match 78.4%; Score 713; DB 5; Length 107;
Best Local Similarity 94.4%; Pred. No. 2.38e-69;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Db 1 dmqmtqttslaelsgdrvtiscrasqdiynlnwyqkpdgtvkllytserlshgvsps 60
Qy 21 DIQMTQTTSLSASLGRVITISCRASQDISSYLNWYQKPDGTETIKLLIYTSRLSHGVS 80
```

```
Db 61 rfsgsgsgtdysltinnleqediatyfcqgkltprtfgggktleik 107
Qy 81 RFSGSGSGTDYSLTINNLEQEDATYFCQGNTLPYTFGGGKLEIN 127
```

```
RESULT 11
ENTRY S38862 #type complete
TITLE Ig kappa chain V region - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
06-Feb-1995
```

```
ACCESSIONS S38862
REFERENCE S37200
#authors Fischer, R.; Voss, A.; Hunziker, W.; Stierhof, Y.D.; Kreuzaler, F.
#submission submitted to the EMBL Data Library, August 1993
#description Production and cloning of TMV-specific monoclonal antibodies.
#accession S38862
#status preliminary
##molecule_type mRNA
##residues 1-108 ##label FIS
#cross-references EMBL:X75854
SUMMARY #length 108 #molecular-weight 11865 #checksum 1422
```

```
Query Match 78.0%; Score 709; DB 11; Length 108;
Best Local Similarity 92.6%; Pred. No. 7.32e-69;
Matches 100; Conservative 6; Mismatches 1; Indels 1; Gaps 1;
```

```
Db 1 dmqmtqttslaelsgdrvtiscrasqdiynlnwyqkpdgtvkllytserlshgvsps 60
Qy 21 DIQMTQTTSLSASLGRVITISCRASQDISSYLNWYQKPDGTETIKLLIYTSRLSHGVS 80
```

```
Db 61 rfsgsgsgtdysltinnleqediatyfcqgntlppwtfggktleik 108
Qy 81 RFSGSGSGTDYSLTINNLEQEDATYFCQGNTLP-YTFGGGKLEIN 127
```

```
RESULT 12 PH0888 #type fragment
ENTRY
```

Jul 8 08:22

US-08-137-117B-29.rpr

9

TITLE Ig light chain V region (anti-CD3) - mouse (fragment)
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 12-Apr-1995
 ACCESSIONS PH0888
 REFERENCE PH0885
 #authors Shalaby, M.R.; Shepard, H.M.; Presta, L.; Rodriguez, M.L.;
 Beverley, P.C.L.; Feldmann, M.; Carter, P.
 #journal J. Exp. Med. (1992) 175:217-225
 #title Development of humanized bispecific antibodies reactive with
 cytotoxic lymphocytes and tumor cells overexpressing the
 HER2 protooncogene.
 #cross-references MUID:92113462
 #accession PH0888
 #molecule_type mRNA
 #residues 1-109 #label SHA
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 SUMMARY #length 109 #checksum 4838

Query Match 77.9%; Score 708; DB 5; Length 109;
 Best Local Similarity 92.5%; Pred. No. 9.70e-69;
 Matches 99; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaaslgdrvtiscrasqdlnynlhwqqkpdgtvkllytstlrlhsgvps 60
 |||||
 Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLIYYTSRLHSGVPS 80

Db 61 kfsgsgtdyaltienlegediatyfcqqntlpwcfaggtkleik 107
 :|||||
 Qy 81 RFSGSGGTDYSLTINNLEQEDIATYFCQQGNTLPYFGGKTLEIN 127

RESULT 13

ENTRY S32188 #type fragment
 TITLE Ig kappa chain V region - mouse (fragment)
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 12-Apr-1995

ACCESSIONS S32188
 REFERENCE S32185
 #authors Izui, S.
 #submission submitted to the EMBL Data Library, February 1993
 #accession S32188
 #status preliminary
 #molecule_type mRNA
 #residues 1-107 #label IZU
 #cross-references EMBL:X70090

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 SUMMARY #length 107 #checksum 7079

Query Match 77.6%; Score 705; DB 5; Length 107;
 Best Local Similarity 91.6%; Pred. No. 2.25e-68;
 Matches 98; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaaslgdrvtiscrasqdlnynlhwqqkpdgtvkllytstlrlhsgvps 60
 |||||
 Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLIYYTSRLHSGVPS 80

Db 61 rfsgsgtdyaltienlegediatyfcqqntlpwcfaggtkleik 107
 |||||
 Qy 81 RFSGSGGTDYSLTINNLEQEDIATYFCQQGNTLPYFGGKTLEIN 127

RESULT 14

Jul 8 08:22

US-08-137-117B-29.rpr

10

ENTRY PLO282 #type fragment
 TITLE Ig light chain V region (45-49, anti p-azophenylarsonate) -
 mouse (fragment)
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Sep-1995
 ACCESSIONS PLO282
 REFERENCE PLO281
 #authors Wysocki, L.J.; Geftter, M.L.; Margolies, M.N.
 #journal J. Exp. Med. (1990) 172:315-323
 #title Parallel evolution of antibody variable regions by somatic
 processes: Consecutive shared somatic alterations in VH
 genes expressed by independently generated hybridomas
 apparently acquired by point mutation and selection rather
 than by gene conversion.

#accession PLO282
 #molecule_type mRNA
 #residues 1-108 #label WYS
 #experimental_source A/J mice
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 KEYWORDS antibody; immunoglobulin
 SUMMARY #length 108 #checksum 960

Query Match 76.7%; Score 697; DB 5; Length 108;
 Best Local Similarity 91.6%; Pred. No. 2.12e-67;
 Matches 98; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaaslgdrvtiscrasqdlnynlhwqqkpdgtvkllytstlrlhsgvps 60
 |||||
 Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQQKPDGTIKLIYYTSRLHSGVPS 80

Db 61 rfsgsgtdyaltienlegediatyfcqqntlpwcfaggtkleik 107
 |||||
 Qy 81 RFSGSGGTDYSLTINNLEQEDIATYFCQQGNTLPYFGGKTLEIN 127

RESULT 15

ENTRY B26405 #type complete
 TITLE Ig kappa chain V region (1F6) - mouse
 ORGANISM #formal name Mus musculus #common name house mouse
 DATE 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 30-Sep-1993

ACCESSIONS B26405
 REFERENCE A90518
 #authors Smith, J.A.; Margolies, M.N.
 #journal Biochemistry (1987) 26:604-612
 #title Complete amino acid sequences of the heavy and light chain
 variable regions from two A/J mouse antigen nonbinding
 monoclonal antibodies bearing the predominant p-azophenyl
 arsonate idiotype.
 #cross-references MUID:87157677

#accession B26405
 #molecule_type protein
 #residues 1-108 #label SMI
 #experimental_source strain A/J
 CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
 SUMMARY #length 108 #molecular-weight 11985 #checksum 1541

Query Match 76.3%; Score 694; DB 5; Length 108;
 Best Local Similarity 92.5%; Pred. No. 4.91e-67;
 Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 1 dlmqtqtsslaaslgdrvtiscrasqdlnynlhwqqkpdgtvkllytstlrlhsgvps 60
 |||||

• • • •

Jul 8 08:22 US-08-137-117B-29.rpf 11

Qy 21 DIQMTQTTSSLASIGDRVTISCRASODISSYLWYQOKPDGTIKLLIYYTSRLHSGVPS 80

Db 61 rfgsgsgtdysltisnlegediatyfcgqgdntlprtfgggkkleik 107

Qy 81 RFGSGSGTDYSLTINNLEQEDIATYFCQQGNLTIFYTGGGKLEIN 127

Search completed: Mon Jul 8 08:32:39 1996
Job time : 28 secs.

Jul 8 08:21

US-08-137-117B-29.rsp

3

```

FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; 63325 CN;

Query Match 78.5%; Score 714; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 1.57e-141;
Matches 101; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Db 1 dlmqtqtsslsaslgdrvtiscrasqdiennlwnyqkpdgtvkliiytsrlhsgvps 60
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLWYQKPDGTIKLIYYTSRLHSGVPS 80
|||||

Db 61 rfsgsgsgtdysltisnleqediattyfcqggnmlprtffgggtkleik 107
Qy 81 RFSGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEIN 127
|||||

RESULT 2
ID KVSU MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP 93G7).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RM 82150934
RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -/- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KWSAR.
DR HSP; P01607; IFAI.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 63046 CN;

Query Match 78.2%; Score 711; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 8.46e-141;
Matches 101; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 1 dlmqtqtsslsaslgdrvtiscrasqdiennlwnyqkpdgtvkliiytsrlhsgvps 60
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLWYQKPDGTIKLIYYTSRLHSGVPS 80
|||||

Db 61 rfsgsgsgtdysltisnleqediattyfcqggnmlprtffgggtkleik 107
Qy 81 RFSGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEIN 127
|||||

RESULT 3
ID KVSU MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (REL. 01, CREATED)

```

Jul 8 08:21

US-08-137-117B-29.rsp

4

```

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP 124E1).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RM 82150934
RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -/- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KWSAR.
DR HSP; P01607; IFAI.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 63856 CN;

Query Match 78.1%; Score 710; DB 4; Length 108;
Best Local Similarity 93.5%; Pred. No. 1.48e-140;
Matches 100; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 1 dlmqtqtsslsaslgdrvtiscrasqdiennlwnyqkpdgtvkliiytsrlhsgvps 60
Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYLWYQKPDGTIKLIYYTSRLHSGVPS 80
|||||

Db 61 rfsgsgsgtdysltisnleqediattyfcqggtklprtffgggtkleik 107
Qy 81 RFSGSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKLEIN 127
|||||

RESULT 4
ID KVSU MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE IG KAPPA CHAIN V-V REGION (HP 123E6).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RM 82150934
RA SIEGELMAN M., CAPRA J.D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
CC -/- ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KWSAR.
DR HSP; P01607; IFAI.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.

```

Jul 8 08:21

US-08-137-117B-29.rsp

5

FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 108 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11989 MW; 64511 CN;

Query Match 77.1%; Score 701; DB 4; Length 108;
 Best Local Similarity 92.5%; Pred. No. 2.30e-138;
 Matches 99; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 1 diqmtqtsslaaslgdrvtiscrasdiynylnwyqkpdgtvkllytyterlhsgvps 60
 Qy 21 DIQMTQTSSLSASIGDRVTISCRASQDISSYLNWYQKPDGTIKLIIYTSRLHSGVPS 80
 Db 61 rfsgsgtdyeltisnleqediatyfcqggymiprtfgggtkleik 107
 Qy 81 RFSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKTLEIN 127

RESULT 5
 ID KV5U MOUSE STANDARD; PRT; 108 AA.
 AC P01648;

DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (HP 91A3).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]

RP SEQUENCE.
 RC STRAIN=A/J;
 RM 82150934
 RA SIEGELMAN M., CAPRA J.D.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 78:7679-7683(1981).
 CC -/- ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR; A01927; KMSAR.
 DR HSSP; P01607; IFAI.
 KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.

FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 108 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11961 MW; 62636 CN;

Query Match 76.8%; Score 698; DB 4; Length 108;
 Best Local Similarity 90.7%; Pred. No. 1.24e-137;
 Matches 91; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Db 1 diqmtqtsslaaslgdrvtiscrasdiynylnwyqkpdgtvkllytyterlhsgvps 60
 Qy 21 DIQMTQTSSLSASIGDRVTISCRASQDISSYLNWYQKPDGTIKLIIYTSRLHSGVPS 80
 Db 61 rfsgsgtdyeltisnleqedistyfcqggalprtfgggtkleik 107
 Qy 81 RFSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKTLEIN 127

Jul 8 08:21

US-08-137-117B-29.rsp

6

RESULT 6
 ID KV5U MOUSE STANDARD; PRT; 108 AA.
 AC P04946;
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (N05-89.4).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]

RP SEQUENCE FROM N.A.
 RM 83271467
 RA KAARTINEN M., GRIFFITHS G.M., MARKHAM A.F., MILSTEIN C.;
 RL NATURE 304:320-324(1983).
 CC -/- ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
 DR EMBL; K00745; WMICKRAO.
 DR HSSP; P01607; IFAI.

KW IMMUNOGLOBULIN V REGION; HYBRIDOMA.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11866 MW; 68556 CN;

Query Match 75.2%; Score 684; DB 4; Length 108;
 Best Local Similarity 88.8%; Pred. No. 3.14e-134;
 Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Db 1 diqmtqtsslaaslgdrvtiscrasdiynylnwyqkpdgtvkllytyterlhsgvps 60
 Qy 21 DIQMTQTSSLSASIGDRVTISCRASQDISSYLNWYQKPDGTIKLIIYTSRLHSGVPS 80
 Db 61 rfsgsgtdyeltisnleqediatyfcqggntlpvtfgggtklxik 107
 Qy 81 RFSGSGTDYSLTINNLEQEDIATYFCQGGNTLPYTFGGGKTLEIN 127

RESULT 7
 ID KV5U MOUSE STANDARD; PRT; 108 AA.
 AC P01643;

DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-V REGION (MOPC 173).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]

RP SEQUENCE.
 RM 76091934
 RA SCHIFF C., FOUCEREAU M.;
 RL EUR. J. BIOCHEM. 59:525-537(1975).
 CC -/- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
 DR PIR; A01926; KWS73.
 DR HSSP; P01607; IFAI.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.

Jul 8 08:21

US-08-137-117B-29.fsp

7

FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 73271 CN;

Query Match 71.8%; Score 653; DB 4; Length 108;
Best Local Similarity 82.2%; Pred. No. 1.04e-126;
Matches 88; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Db 1 dimgtqtsslaealqdrvticcasagignylbwyqkqpdvktlllytsslhsgvps 60
|||||
Qy 21 DIQMTQTSSLSASLGRVITISCRASQDISSYINWYQKRPDGTIKLLIYYTSLHSGVPS 80
|||||

Db 61 rfsgsgsgtdyeltisblzpzbiatyccqyqsklprtfsgggtkleik 107
|||||

Qy 81 RFSGSGSGTDSLNNLEQEDIATYFCQGNLTLPYTFGGTKLEIN 127
|||||

RESULT 8
ID KV1W HUMAN STANDARD; PRT; 129 AA.

AC P04431;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-I REGION (WALKER).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RM 85014148
RA KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
RL NUCLEIC ACIDS RES. 12:6995-7006(1984).
DR EMBL; X00965; HSVK01.
DR PIR; A01883; K1RWK.
DR HSP; P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION (WALKER).
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 120 129 FRAMEWORK 4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; 94965 CN;

Query Match 69.0%; Score 627; DB 4; Length 129;
Best Local Similarity 68.5%; Pred. No. 2.04e-120;
Matches 87; Conservative 22; Mismatches 18; Indels 0; Gaps 0;

Db 3 mrvpaqlgllllwlgarcdiqtqpslaasvqdrvtitcrasgeinylnwyqkqp 62
| :|||:||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 WVSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGRVITISCRASQDISSYINWYQKRP 60
|||||

Db 63 gkapklliyaaslsqvtarfgsgsgtdftltisllqpdeatyccqysetlittfgq 122
: ||||| :| :||| |||||:|||||:|||||:|||||:|||||:|||||:|||||

Jul 8 08:21

US-08-137-117B-29.fsp

8

Qy 61 DGTIKLLIYYTSLHSGVPSRFSGSGGTDSLNNLEQEDIATYFCQGNLTLPYTFGG 120
Db 123 qtrleik 129
||:||||
Qy 121 GTKLEIN 127

RESULT 9
ID KV5G MOUSE STANDARD; PRT; 130 AA.
AC P01639; P01640;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RM 79221900
RA SEIDMAN J.G., MAX E.E., LEDER P.;
RL NATURE 280:370-375(1979).
RN [2]
RP SEQUENCE OF 1-33.
RM 77148916
RA BURSTEIN Y., SCHECHTER I.;
RL PROC. NATL. ACAD. SCI. U.S.A. 74:716-720(1977).
RN [3]
RP SEQUENCE OF 23-130.
RM 67056897

RA GRAY W.R., DREYER W.J., HOOD L.;
RL SCIENCE 155:465-467(1967).
CC -!- THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE SYSTEM DIRECTED BY
CC -!- MENA ISOLATED FROM MYELOMA POLYSOMES.
CC -!- THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01922; KVMSM4.
DR HSP; P01607; 6FAB.
KW IMMUNOGLOBULIN V REGION; SIGNAL; BENCE-JONES PROTEIN.
FT SIGNAL 1 22
FT CHAIN 23 116 IG KAPPA CHAIN V-V REGION (MOPC 41).
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 120 129 FRAMEWORK 4.
FT VARIANT 1 2 MISSING (IN 25% OF THE MOLECULES).
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 130 130
SQ SEQUENCE 130 AA; 14311 MW; 96159 CN;

Query Match 68.0%; Score 618; DB 4; Length 130;
Best Local Similarity 70.1%; Pred. No. 3.05e-118;
Matches 89; Conservative 18; Mismatches 20; Indels 0; Gaps 0;

Db 3 mrapaqiflllllfgqtrcdiqtqpslaasvqdrvtitcrasgeinylnwqlqep 62
| :|||:||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 WVSSAQFLGLLLCFQGRCDIQMTQTSSLSASLGRVITISCRASQDISSYINWYQKRP 60
|||||

Db 63 dgtikrliyatssldsgvvpkrfsgsgsgtdftltisllqpdeatyccqysetlittfgq 122
|||||

Qy 61 DGTIKLLIYYTSLHSGVPSRFSGSGGTDSLNNLEQEDIATYFCQGNLTLPYTFGG 120

1 di0mt0tpsslsasldrvsiscrasqdlsqylfwqackpqqppklliyvrsltnqvdp 60

Query Match 62.0%; Score 564; DB 4; Length 108;

Query Match

Jul 8 08:21

US-08-137-117B-29.rsp

13

Best Local Similarity 72.6%; Pred. No. 3.01e-105;
Matches 77; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

Db 1 dmqmtqpslasvdrvtitcasqdiikynwyqgtpgkapklllyeanlqagvps 60

Qy 21 DIQMTQTSSLSASLGDRVTISCRASQDISSYINWYQKRPDGTIKLLIYYTSLRLHSGVPS 80

Db 61 rfsqsgsgtdyftisalpeditatycqayqslpytfgqgkklqi 106

Qy 81 RESGSGTDSLTLNNLEQEDIATYFCQGNTLPYTFGGTKLEI 126

RESULT 15

ID KVLJ HUMAN STANDARD; PRT; 117 AA.

AC P01602;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

DE IG KAPPA CHAIN PRECURSOR V-I REGION (HK102) (FRAGMENT) .

OS HOMO SAPIENS (HUMAN) .

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RM 81098966

RA BENTLEY D.L., RABBITTS T.H.;

RL NATURE 288:730-733(1980) .

DR ENBL; 200001; HSI6K3.

DR PIR; A01882; KIHU12.

DR HSSP; P01607; 1DFB.

KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT SIGNAL 1 22

FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION (HK102) .

FT DOMAIN 23 45 FRAMEWORK 1.

FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 57 71 FRAMEWORK 2.

FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 79 110 FRAMEWORK 3.

FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING 3.

FT DISULFID 45 110 BY SIMILARITY.

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12768 MW; 80156 CN;

Query Match

Best Local Similarity 61.7%; Score 561; DB 4; Length 117;

Matches 75; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

Db 3 mrvpaqlgllllwlpgakcdlqmtqpsltsasvdrvtitcrasqslawlyqkqp 62

Qy 1 MWSAQLGLLLLCFCQCTRCDTQMTQTSSLSASLGDRVTISCRASQDISSYINWYQKRP 60

Db 63 gkapklliydasslesgvpfrfsqsgtftltisslpddfatvycqq 112

Qy 61 DGTIKLLIYYTSLRLHSGVPSRFSGSGTDSLTLNNLEQEDIATYFCQQ 110

Search completed: Mon Jul 8 08:31:55 1996
Job time : 13 secs.

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPsrch pp protein - protein database search, using Smith-Waterman algorithm

```
Run on: Mon Jul 8 08:32:56 1996; MasPar time 4.21 Seconds
250.053 Million cell updates/sec
```

Tabular output not generated.

Title: >US-08-137-117B-29

Description: (1-127) from US08137117B.ppt

Perfect Score: 909
Sequence: 1 MVSSAQFLGLLLLCFQTRC.....CQCGNTIPYTFGGGTKLEIN 127

Scoring table: PAM 150
Gap 11

Searched: 70887 seqs, 8282111 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:
a-geneseq22
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14

Statistics: Mean 30.127; Variance 164.919; scale 0.183

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query			DB	ID	Description	Pred. No.
	No.	Score	Match Length				
1	909	100.0	127	6	R28670	pPM-k3 protein produc	1.06e-59
2	879	96.7	131	14	R48553	MAB SCH94.03 light ch	2.18e-57
3	876	96.4	127	6	R32121	Anti-CD4 antibody MT	3.72e-57
4	860	94.6	128	5	R09426	ME4 Light Chain V Reg	6.37e-56
5	853	93.8	127	8	R32965	Mouse C4G1 Ig light-c	2.20e-55
6	826	90.9	127	6	R29010	p146-C3 protein produ	2.65e-53
7	818	90.0	127	2	R12359	Light (kappa) chain v	1.09e-52
8	817	89.9	126	9	R12237	Mouse Mab 1C11 L chai	1.30e-52
9	814	89.5	124	9	R47206	Human/murine IL-1 chi	2.22e-52
10	802	88.2	128	7	R33257	Rat immunoglobulin L	1.86e-51
11	786	86.5	128	10	R53340	KM461 H chain variabl	3.16e-50
12	708	77.9	107	6	R30768	Murine anti-CD3 MAb v	3.06e-44

13	694	76.3	302	11	R60206	Bispecific CD3-L6FvIg	3.61e-43
14	686	75.5	219	9	R30776	HY216-158 murine anti	1.48e-42
15	681	74.9	129	9	R407207	Human/murine IL-1 chi	3.56e-42
16	678	74.6	273	10	R52865	Anti-influenza N10 sc	6.04e-42
17	661	72.7	129	2	R11057	Feline immunoglobulin	1.20e-40
18	652	71.7	126	6	R29013	pUC-RVH-PM1a.	5.86e-40
19	652	71.7	126	6	R29015	pUC-RV1-PM1a.	5.86e-40
20	645	71.0	129	13	R57482	Humanized 1308F VL.	2.01e-39
21	641	70.5	234	3	R13050	CD4-specific IgG8F graf	4.05e-39
22	625	68.8	214	7	R43338	Completely humanised	6.73e-38
23	621	68.3	233	6	R30777	pH52-9.0 humanised mu	1.36e-37
24	619	68.1	128	1	R06252	Variable region of mu	1.93e-37
25	617	67.9	129	6	R30880	pXOM2.	2.74e-37
26	617	67.9	130	13	R75394	Anti-interleukin-1-al	2.74e-37
27	615	67.7	146	4	R30251	Sequence of the leade	3.89e-37
28	614	67.5	234	7	R38162	Sequence of the kappa	4.64e-37
29	612	67.3	128	12	R06027	ME1-14 light chain va	6.59e-37
30	612	67.3	138	12	R62881	Murine anti-human ath	6.59e-37
31	609	67.0	128	10	R53332	KM-603 light chain.	1.11e-36
32	607	66.8	236	8	R42065	Human anti-Hbs light	1.58e-36
33	602	66.2	142	14	R81311	Rat monoclonal antibody	3.80e-36
34	598	65.8	117	7	R38651	Human V-kappa fragmen	7.67e-36
35	598	65.8	117	12	R62931	Human V-kappa vk65.15	7.67e-36
36	597	65.7	125	6	R30820	YFC51.1.1 light chain	9.14e-36
37	596	65.6	107	6	R30769	huxCD3v9, humanised m	1.09e-35
38	592	65.1	234	3	R20508	Light chain of 306 an	2.19e-35
39	586	64.5	129	13	R65018	93KA9 anti-VariCella	6.27e-35
40	585	64.4	128	12	R64234	Humanized antibody L2	7.47e-35
41	585	64.4	128	13	R64264	CDR-grafted I243-g12	7.47e-35
42	581	63.9	128	10	R54053	Sequence of the VL re	1.50e-34
43	575	63.3	109	9	R47041	Sequence of the conse	4.30e-34
44	573	63.0	107	13	R77302	Variable light chain	6.10e-34
45	573	63.0	128	12	R64233	Humanized antibody L2	6.10e-34

ALIGNMENTS

RESULT	1	
ID	R28670 standard; Protein; 127 AA.	
AC	R28670;	
DT	30-MAR-1993 (first entry)	
DE	pPM-k3 protein product.	
DE	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H; H;	
KW	heavy chain; variable region; mouse; monoclonal; hybridoma; PMI;	
KW	plasmid; pPM-k3; pPM-h1.	
KW	Synthetic.	
OS		
Key	Location/Qualifiers	
FFH	Peptide	
FT	1..20	
FT	/note= "Signal peptide"	
FT	Protein	
FT	21..127	
FT	/note= "Mature peptide"	
PN	W09219759-A.	
PD	12-NOV-1992.	
PF	24-APR-1992; J00544.	
PR	25-APR-1991; JP-095476.	
PR	19-FEB-1992; JP-032084.	
PA	(CHUS) CHUGAI SEIYAKU KK.	
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;	
DR	WFI; 92-398882/48.	
DR	N-PSDB; Q30755.	
DR	Reconstituted human antibody to human interleukin-6 receptor -	
PT	has low antigenicity and contains mouse V-region complementarity	
PT	determining regions	
PT	disclosure; Page 121-122; 207bp; Japanese.	

Jul 8 08:22

US-08-137-117B-29:ag

3

CC The sequences given in R28670-71 were encoded by plasmids which were used in example to illustrate the production of a human antibody which recognises human interleukin-6 receptor (IL-6R). The antibody comprises light (L) chain and heavy (H) chain variable regions which were derived from a mouse monoclonal antibody produced from the hybridoma PM1 which contained the plasmids pPM-k3 and pPM-h1.

SQ Sequence 127 AA;
Query Match 100.0%; Score 909; DB 6; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.06e-59;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 mvssaqlglilllcfqgtrcdiqmtqtasleaslgdrvtiscrasqdiessylwnyqkqp 60
Qy 1 WVSSAQFLGLLLCFQGTCTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKQP 60
Db 61 dgtikllyvtterlshgvsprfsgsgtdysltinnleqediatyfcqgntlpytfgg 120
Qy 61 DGTIKLIIYVTSRLHSGVPSRFSGSGTDSLITINNLEQEDIAITYFCQGNLTPLYTFGG 120
Db 121 gtklein 127
Qy 121 GTKLEIN 127

RESULT 2

ID R84553 standard; Protein; 131 AA.
AC R84553;
DT 02-FEB-1996 (first entry)
DE Mab SCH94.03 light chain.
KW Monoclonal antibody; MAb; SCH94.03; hybridoma; central nervous system; CNS; demyelination; multiple sclerosis; neural disease; therapeutic.
OS Mus sp.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Leader_peptide
FT Region 44..54
FT /label= CDR1
FT Region 70..76
FT /label= CDR2
FT Region 109..117
FT /label= CDR3
FT Region 116..128
FT /label= Joining_region
FT Region 129..131
FT /label= C-kappa_region
PN W09530004-A1.
PD 09-NOV-1995.
PF 27-APR-1995; US5262.
PR 29-APR-1994; US-236520.
PA (MAYO-) MAYO FOUNDATION.
PI Miller DJ, Rodriguez M;
DR WPI; 95-393077/50.
DR N-PSDB; T05311.
PT Monoclonal antibodies which stimulate central nervous system
PT re-myelination - are produced by hybridoma ATCC CRL 11627, for
PT treating multiple sclerosis, and viral or post-neural diseases of
PT the CNS.
PS Disclosure; Page 36-37; 63pp; English.
CC Hybridoma ATCC CRL 11627 was obtained from a SJL/J mouse injected with
CC spinal cord homogenate from a mammal uninfected with any
CC demyelinating disease. The hybridoma produced a monoclonal antibody
CC (SCH94.03) useful in promoting CNS remyelination. The SCH94.03
CC light chain amino acid sequence is given in R84553.

Jul 8 08:22

US-08-137-117B-29:ag

4

SQ Sequence 131 AA;
Query Match 96.7%; Score 879; DB 14; Length 131;
Best Local Similarity 95.3%; Pred. No. 2.18e-57;
Matches 121; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db 1 mmssaqlglilllcfqgtrcdiqmtqtasleaslgdrvtiscrasqdiessylwnyqkqp 60
Qy 1 WVSSAQFLGLLLCFQGTCTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKQP 60
Db 61 dgtvkllyvtterlshgvsprfsgsgtdysltinnleqediatyfcqgntlpytfgg 120
Qy 61 DGTIKLIIYVTSRLHSGVPSRFSGSGTDSLITINNLEQEDIAITYFCQGNLTPLYTFGG 120
Db 121 gtleik 127
Qy 121 GTLEIN 127

RESULT 3

ID R32121 standard; Protein; 127 AA.
AC R32121;
DT 02-JUN-1993 (first entry)
DE Anti-CD4 antibody MT 15.1 light chain variable region.
KW Immunosuppression; tissue transplantation; graft; L chain; V region;
KW T-helper cell inhibition; transplant rejection; MAb;
KW interleukin-2 receptor.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= signal
FT Region 21..115
FT /label= Variable
FT Region 116..127
FT /label= J2
PN DE4143214-A.
PD 28-JAN-1993.
PF 30-DEC-1991; 143214.
PR 25-JUL-1991; DE-124759.
PR 30-DEC-1991; DE-143214.
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PI Kaluza B, Rietmueller G, Scheuer W, Weidle U;
DR WPI; 93-037582/05.
DR N-PSDB; Q36607.
PT Synergistic antibody compn. for use as immunosuppressant -
PT comprises monoclonal anti-CD4 antibodies and monoclonal anti-IL2R
PT alpha- or anti-IL2R beta antibodies
PS Claim 5; Page 9; 18pp; German.
CC This sequence is the light chain variable region of a preferred
CC anti-CD4 monoclonal antibody for use in the claimed synergistic
CC composition. Mab MT 15.1 is deposited as clone 15-1/P3/14 (ECACC
CC 90090705). The anti-CD4 antibody is used with at least one anti-IL2R
CC alpha or beta antibody. Individually the antibodies are strongly
CC inhibiting and when used together their immunosuppressive properties
CC are improved; they synergistically inhibit T-helper cell
CC proliferation to effectively inhibit transplant rejection at low
CC doses without significantly reducing the general immune response.
CC See also Q36608-Q36616.
SQ Sequence 127 AA;

Query Match 96.4%; Score 876; DB 6; Length 127;
Best Local Similarity 92.9%; Pred. No. 3.72e-57;
Matches 118; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
Db 1 mmssaqlglilllcfqgtrcdiqmtqtasleaslgdrvtiscrasqdiessylwnyqkqp 60

Jul 8 08:22

US-08-137-117B-29.rag

5

```
Qy 1 MVSSAQFLGILLLCFQCTRCDIQMTQTSSLSASLGRVVTISCRASQDISSYLNWYQKP 60
Db 61 dqtvkliiyterlshgvsrfsqsgtdysltitnleqdvatyfcqgntlpytfqg 120
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQGGNTLPYTFGG 120
Db 121 gtkleik 127
Qy 121 GTKLEIN 127
```

RESULT 4

```
ID R09426 standard; Protein; 128 AA.
AC R09426;
DE 04-MAR-1993 (first entry)
ME4 Light Chain V Region (mouse).
KW Monoclonal antibody; chimera; light; heavy; chain; constant;
KW variable; antigen; diagnosis; cancer; tumour.
QS Mus musculus.
PN W09002569-A.
PD 22-MAR-1990.
PF 06-SEP-1989; U03852.
PR 06-SEP-1988; US-240624.
PR 08-SEP-1988; US-241744.
PR 13-SEP-1988; US-243739.
PR 04-OCT-1988; US-253002.
PR 19-JUN-1989; US-367641.
PR 21-JUL-1989; US-382768.
PA (ITGE-) INT GENETIC ENG INC.
PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
DR WPI; 90-115825/15.
DR N-PSDB; Q08608.
CC Chimeric mouse-human antibodies - prepd. using genes coding for
PT constant human region murine variable region, esp. to 3 tumour
PT antigen
PS Claim 13; Page 123 + Fig 29; 173pp; English.
CC The sequence is used in the prodn. of a chimeric antibody mol.
CC comprising two light chains and two heavy chains, each having a
CC constant region (human) and a variable region (murine) having
CC specificity to an antigen bound by murine monoclonal antibody
CC (MAB) ME4. The chimeric antibodies can be used for any purpose for
CC which the original murine MABs can be used, with the advantage that
CC they are more compatible with the human body. They are esp. used for
CC the diagnosis and treatment of cancer.
SQ Sequence 128 AA;
```

```
Query Match 94.6%; Score 860; DB 5; Length 128;
Best Local Similarity 92.9%; Pred. No. 6.37e-56;
Matches 118; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
```

```
Db 1 mmsaqlgllllcfcgqtrcdlqmtqtsslsaslgdrvtiscrasqdttylnwyqkp 60
Qy 1 MVSSAQFLGILLLCFQCTRCDIQMTQTSSLSASLGRVVTISCRASQDISSYLNWYQKP 60
Db 61 dqtvkliiyterlshgvsrfsqsgtdysltitnleqdvatyfcqgntlpytfqg 120
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQGGNTLPYTFGG 120
Db 121 gtkleik 127
Qy 121 GTKLEIN 127
```

Jul 8 08:22

US-08-137-117B-29.rag

6

```
RESULT 5
ID R39265 standard; Protein; 127 AA.
AC R39265;
DE 29-NOV-1993 (first entry)
DE Mouse C4G1 Ig light-chain.
KW Immunoglobulin; L-chain; platelet membrane glycoprotein; GPIIa/IIb;
KW monoclonal antibody; platelet agglutination; humanised antibody.
OS Synthetic.
```

```
FN Key Location/Qualifiers
FT Peptide 1..21
FT /label= signal_peptide
FT Protein 22..127
FT /label= light_chain
FT Region 44..54
FT /label= complementarity_determining_region_1
FT Region 70..76
FT /label= CDR 2 109..117
FT /label= CDR 3
FT W09313133-A.
PD 08-JUL-1993.
PF 15-DEC-1992; J01630.
PR 20-DEC-1991; US-812111.
PR 09-JUN-1992; US-895952.
PR 11-SEP-1992; US-944159.
PA (PROT-) PROTEIN DESIGN LABS INC.
PA (YAMA ) YAMANOUCHI PHARM CO LTD.
PI Co MS, Tso JY;
DR WPI; 93-227275/28.
DR N-PSDB; Q45662.
PT Compsn. contg. immunoglobulin specific for the GP-IIb and -IIIa
PT protein - for treating disorders related to vascular thrombosis
PS Disclosure; Fig 2A; 54pp; Japanese.
CC This is the sequence of the mouse C4G1 immunoglobulin light
CC chain. See R39266 for the heavy chain sequence. The antibody is
CC specific for the GPIIa/IIb protein and inhibits platelet
CC agglutination. The Ig is thus useful in the treatment of
CC thrombosis.
SQ Sequence 127 AA;
```

```
Query Match 93.8%; Score 853; DB 8; Length 127;
Best Local Similarity 92.1%; Pred. No. 2.20e-55;
Matches 117; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
```

```
Db 1 mmsaqlgllllcfcgqtrcdlqmtqtsslsaslgdrvtiscrasqdttylnwyqkp 60
Qy 1 MVSSAQFLGILLLCFQCTRCDIQMTQTSSLSASLGRVVTISCRASQDISSYLNWYQKP 60
Db 61 dqtvkliiyterlshgvsrfsqsgtdysltitnleqdvatyfcqgntlpytfqg 120
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGCTDYSLTINNLEQEDIATYFCQGGNTLPYTFGG 120
Db 121 gtkleik 127
Qy 121 GTKLEIN 127
```

RESULT 6

```
ID R29010 standard; Protein; 127 AA.
AC R29010;
DE 30-MAR-1993 (first entry)
DE pl46-k3 protein product.
KW Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;
KW heavy chain; variable region; mouse; monoclonal; hybridoma; AUK146-15;
```

Jul 8 08:22

US-08-137-117B-29.rag

7

KW plasmid; p146-k3; p146-h1.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..127
FT /note= "Mature peptide"
FN W09219759-A.
PD 12-NOV-1992.
PF 24-APR-1992; J00544.
PR 25-APR-1991; JP-095476.
PR 19-FEB-1992; JP-032084.
PA (CHUS) CHUGAI SEIYAKU KK.
PI Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;
DR WPI; 92-398882/48.
DR N-PSDB; Q30759.
PT Reconstituted human antibody to human interleukin-6 receptor -
PT has low antigenicity and contains mouse V-region complementarity
PT determining regions
PS Disclosure; Page 127-128; 207pp; Japanese.
CC The sequences given in R29010-11 were encoded by plasmids which were
CC used in example to illustrate the production of a human antibody which
CC recognises human interleukin-6 receptor (IL-6R). The antibody
CC comprises light (L) chain and heavy (H) chain variable regions which
CC were derived from a mouse monoclonal antibody produced from the
CC hybridoma AUK146-15 which contained the plasmids p146-k3 and p146-h1.
SQ Sequence 127 AA;

Query Match 90.9%; Score 826; DB 6; Length 127;
Best Local Similarity 89.8%; Pred. No. 2.65e-53;
Matches 114; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Db 1 mvstpqflglvfcfgtcdiqtqtsslsaslgdrvtiscrasqgsniynwqqkp 60
Qy 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
Db 61 dgtvkllyttsrlhsqgsfsgsgtdyeltisnleqediayfcqggytpwtfgg 120
Qy 61 DGTIKLLIYTRSLHSQGSFSGSGTDYSLTINNLEQEDIATYFCQGNTLPYTFGG 120
Db 121 gtkleik 127
Qy 121 GTKLEIN 127

RESULT 7

ID R12359 standard; Protein; 127 AA.
AC R12359;
DT 15-AUG-1991 (first entry)
DE Light (kappa) chain variable region of murine 1C11 immunoglobulin.
KW Chimeric antibodies; Immunoconjugates; HIV; AIDS.
OS Mus musculus.
PN W09107493-A.
PD 30-MAY-1991.
PF 13-NOV-1990; U06615.
PR 13-NOV-1989; US-433730.
PA (XOMA-) XOMA CORP.
PA (GREC) GREEN CROSS CORP.
PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
DR WPI; 91-178044/24.
DR N-PSDB; Q12061.
PT New chimeric mouse-human antibodies - used to detect, kill and
PT remove HIV-1 antigen from sample
PS Disclosure; fig 13; 107pp; English.

Jul 8 08:22

US-08-137-117B-29.rag

8

CC This is the light (kappa)- chain variable (V) region of a mouse
CC monoclonal antibody (MAb), 1C11, and is specific for an HIV-1
CC viral antigen. It is used in the construction of a chimeric
CC MAb comprising heavy and light chains having murine V regions
CC and human C regions. The chimeric MABs are more effective than
CC murine MAB 1C11 since they have an increased compatibility in
CC humans. The heavy and light chain V-regions are joined by
CC manipulating their respective joining (J) regions, to generate
CC restriction enzyme recognition sites. The chimeric MABs can be
CC used as immunoconjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV.
CC See also Q12056-60 and Q12062-63.
SQ Sequence 127 AA;

Query Match 90.0%; Score 818; DB 2; Length 127;
Best Local Similarity 89.0%; Pred. No. 1.09e-52;
Matches 113; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Db 1 mmsaqlglvlllcfqgtcdiqtqtsslsaslgdrvtiscrasqgsniynwqqkp 60
Qy 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60
Db 61 dgtvkllyttsrlhsqgsfsgsgtdyeltisnleqediayfcqggytpwtfgg 120
Qy 61 DGTIKLLIYTRSLHSQGSFSGSGTDYSLTINNLEQEDIATYFCQGNTLPYTFGG 120
Db 121 gtkleik 127
Qy 121 GTKLEIN 127

RESULT 8

ID R12237 standard; Protein; 126 AA.
AC R12237;
DT 19-AUG-1991 (first entry)
DE Mouse MAB 1C11 L chain V region.
KW HIV-1; chimera.
OS Mus sp.
PN W09107494-A.
PD 30-MAY-1991.
PF 13-NOV-1990; U06627.
PR 13-NOV-1989; US-433703.
PA (XOMA-) Xoma Corp.
PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
DR WPI; 91-178106/24.
DR N-PSDB; Q12017.
PT New chimeric mouse human antibodies - used in treatment, diagnosis
PT and prophylaxis of HIV infections.
PS Disclosure; Fig 13; 108pp; English.
CC The mouse VL gene product may be used to produce chimeric mouse-
CC human Abs against HIV-1 comprising human Ig constant regions and
CC murine variable regions. These novel sequence are useful in
CC treatment, diagnosis and prophylaxis of HIV infections, and may be
CC produced by a bacterial, yeast or mammalian expression system.
SQ Sequence 126 AA;

Query Match 89.9%; Score 817; DB 2; Length 126;
Best Local Similarity 89.7%; Pred. No. 1.30e-52;
Matches 113; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Db 1 mmsaqlglvlllcfqgtcdiqtqtsslsaslgdrvtiscrasqgsniynwqqkp 60
Qy 1 MVSSAQFLGLLLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDISSYLNWYQKP 60

—

'67

Jul 8 08:22

US-08-137-117B-29.rag

11

OS Mus musculus.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label=eig_peptide
PW AU9346181-A.
PD 17-MAR-1994.
PR 07-SEP-1992; JP-238452.
PA (KYOM) KYOMA HAKKO KOGYO KK.
PI Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
PI Shitara K;
DR WPI; 94-126857/16.
DR N-PSDB; Q45438.
PT Humanised antibody specific for ganglioside GM2 - used for
PT producing a cytotoxic effect on cancers such as melanoma,
PT neuroblastoma and glioma.
PS Reference example 2; Page 115-116; 191pp; English.
CC Example 2 describes the construction of the vector pCh1641HA1
CC for chimeric human antibody H chain expression.
CC mRNA from mouse anti-GD3 monoclonal Ab KM641-producing cells
CC was isolated and KM641 H and L chain cDNAs isolated.
CC The base sequences of the Ig variable regions in KM641
CC H chain cDNA (pKM641HA3) and KM641 L chain cDNA (pKM641LA2)
CC are given in Q45438-39. A KM641-derived chimeric human
CC Ab H chain expression vector was constructed by joining
CC the H chain variable region gene from pKM641HA3 to a
CC vector for chimeric human Ab H chain expression using
CC the synthetic DNAs given in Q63439 and Q63440.
SQ Sequence 128 AA;

Query Match 86.5%; Score 786; DB 10; Length 128;
Best Local Similarity 84.3%; Pred. No. 3.16e-50;
Matches 107; Conservative 12; Mismatches 8; Indels 0; Gaps 0;

Db 1 mmsaaqflgllllcfqtrcdiqtatasepalslgrvtiscsasqdiynlwyqkq 60
Qy 1 MYSSAQFLGILLLCFQGTGTRCDIQMTTSSLSASLGDRVTISCRASQDISSYLWYQKQ 60
Db 61 dgtvkllyfsenlhsgvparfsggsgtdyeltisnleqdiatyfchqysklptegg 120
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGSDTYSLTINWLEQDIATYFCQGGNTLPTFEGG 120
Db 121 gtleik 127
Qy 121 GTRLEIN 127

RESULT 12
ID R30768 standard; protein; 107 AA.
AC R30768;
DT 12-MAY-1993 (first entry)
DE Murine anti-CD3 MAb UCHT1 light chain variable domain.
KW Humanisation; rapid; monoclonal antibody; muxCD3.
OS Mus musculus.
PN W09222653-A.
PD 23-DEC-1992.
PF 15-JUN-1992; U05126.
PR 14-JUN-1991; US-715272.
PA (GETH) GENENTECH INC.
PI Carter PJ, Presta IG.
DR WPI; 93-018139/02.
PT Humanisation of antibodies - by molecular modelling of the variable
PT domains and alteration by gene conversion mutagenesis
PS Disclosure; Fig 5; 126pp; English.

Jul 8 08:22

US-08-137-117B-29.rag

12

CC The sequence is that of the light chain variable domain of murine
CC anti-CD3 monoclonal antibody UCHT1 (muxCD3, Shalaby 1992).
SQ Sequence 107 AA;
Query Match 77.9%; Score 708; DB 6; Length 107;
Best Local Similarity 92.5%; Pred. No. 3.06e-44;
Matches 99; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Db 1 digmtqtteslaaslgdrvtiscsasqdiynlwyqkpdgtvkllytserlhsgvps 60
Qy 21 DIQMTQTTSLSASLGDRVTISCRASQDISSYLWYQKPDGTIKLLIYTSRLHSGVPS 80
Db 61 kfsgsgtdyeltisnleqdiatyfchqggntlptwfaggtkleik 107
Qy 81 RFSGSGSDTYSLTINWLEQDIATYFCQGGNTLPTYFGGKLEIN 127

RESULT 13
ID R60206 standard; Protein; 302 AA.
AC R60206;
DT 14-MAR-1995 (first entry)
DE Bispecific CD3-L6Fvlg antibody derivative.
KW fusion protein; recombinant bispecific single chain antibody;
KW helical peptide linker; anti-L6 antibody; tumour cell antigen;
KW anti-CD3 antibody; variable region.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label=L6_VL_leader
FT Region 24..271
FT /label=CD3_VL-VH fusion
FT Region 134..148
FT /label=(Gly4Ser)3 linker
FT Region 272..274
FT /label=hinge
FT Region 275..302
FT /label=Fv_helical_linker
PW EP-610046-A.
PD 10-AUG-1994.
PF 31-JAN-1994; 300692.
PR 01-FEB-1993; US-013420.
PR 13-SEP-1993; US-121054.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
PI Bajorath J, Fell PH, Gilliland LK, Hayden MS, Ledbetter JA;
PI Linsley PS;
DR WPI; 94-250885/31.
DR N-PSDB; Q81076.
PT Expression vector encoding bispecific fusion protein - having
PT binding domains for separate targets joined by helical peptide,
PT useful e.g. for diagnosis and treatment
PS Example 1; Fig 11 and Page 29-31; 50pp; English.
CC The VL and VH sequences of the anti-CD3 hybridoma G19-4 were
CC amplified by PCR methods. A gene fusion was constructed from the
CC two amplified domains and a (Gly4Ser)3 linker. The amino
CC terminus of the VL-VH fusion cassette was fused at the SalI site to
CC the L6 light chain variable region leader peptide and the
CC carboxy-terminus was fused directly to the hinge region of the Fc
CC domain at the BclI site and/or to a short "helical" peptide linker
CC to construct the bispecific CD3-L6Fvlg antibody derivative. The
CC variable regions for L6 were fused in frame to the opposite end of
CC the helical linker (not included in R60206).
SQ Sequence 302 AA;

Query Match 76.3%; Score 694; DB 11; Length 302;

Jul 8 08:22

US-08-137-117B-29rag

13

Best Local Similarity 93.3%; Pred. No. 3.61e-43;
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Db 24 diqmqttslaslsgdrvtisrcasqdirnylnwyqkqdgktvkllytstlhagvps 83
Qy 21 DIQMTQTTSLSASLGDRTVTISCRASQDISSYLNWYQKQPDGTIKLLIYTSRLHSGVPS 80
Db 84 rfsgegsqtdysltianlqpediatyfcqggntlpwtfgggtkl 127
Qy 81 RFSGSGSDTYSLTINNLEQEDIATYFCQGGNTLPYTFGGGTKL 124

RESULT 14

ID R30776 standard; protein; 214 AA.
AC R30776;
DT 12-MAY-1993 (first entry)
DE H52L6-158 murine anti-CD18 antibody light chain.
KW Humanisation; rapid; monoclonal antibody.
OS Mus musculus.
PN W09222653-A.
PD 23-DEC-1992.
PF 15-JUN-1992; U05126.
PR 14-JUN-1991; US-715272.
PA (GETH) GENENTECH INC.
PI Carter PJ, Presta LG.
DR WPI; 93-018139/02.
PT Humanisation of antibodies - by molecular modelling of the variable
PT domains and alteration by gene conversion mutagenesis
PS Disclosure; Fig 68; 126pp; English.
CC The sequence is that of the light chain of murine anti-CD18
CC antibody H52L6-158.
SQ Sequence 214 AA;

Query Match 75.5%; Score 686; DB 6; Length 214;
Best Local Similarity 88.8%; Pred. No. 1.48e-42;
Matches 95; Conservative 10; Mismatches 2; Indels 0; Gaps 0;
Db 1 dvqmqttslaslsgdrvtisrcasqdirnylnwyqkqngtvtkllytstlhagvps 60
Qy 21 DIQMTQTTSLSASLGDRTVTISCRASQDISSYLNWYQKQPDGTIKLLIYTSRLHSGVPS 80
Db 61 rfsgegsqtdysltianlqpediatyfcqggntlpwtfgggtkveik 107
Qy 81 RFSGSGSDTYSLTINNLEQEDIATYFCQGGNTLPYTFGGGTKLEIN 127

RESULT 15

ID R47207 standard; Protein; 129 AA.
AC R47207;
DT 09-AUG-1994 (first entry)
DE Human/murine IL-1 chimeric antibody VL.
KW Probe; chimeric; recombinant; antibody; human; interleukin-1; IL-1;
KW light; L; chain; constant; region; variable; mouse; anti-human;
KW graft; CDR; complementarity determining region; heavy; H;
KW inflammatory disease; arteriosclerosis; detection;
KW diffused intravascular coagulation; leukemia.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..129
FT /note= "Mature protein"
PN W09402627-A.
PD 03-FEB-1994.

Jul 8 08:22

US-08-137-117B-29rag

14

PF 08-JUL-1993; J00941.
PR 16-JUL-1992; JP-189248.
PA (SAKA) OTSUKA PHARM CO LTD.
PI Hirai Y, Nishida T, Onoto Y, Owens RJ;
DR WPI; 94-048885/06.
DR N-PSDB; Q56068.
PT Mouse/human chimeric antibody against human interleukin-1 - for
PT treatment of diseases in which production of interleukin-1 is
PT abnormal, and for diagnostic imaging of interleukin-1 production
PT sites in vivo
PS Claim 2; Fig 10; 58pp; Japanese.
CC The sequences given in R47205-08 represent the light and heavy chain,
CC variable and constant regions of a chimeric recombinant antibody
CC against human interleukin-1 (IL-1). The antibody has a light (L)
CC chain in which the constant region is that of a human antibody and
CC the variable region is from a mouse anti-human IL-1 antibody or is a
CC mouse-human graft containing the CDR regions of mouse anti-human IL-1
CC antibody, and a heavy (H) chain in which the constant region is that
CC of a human antibody and the variable region is from a mouse anti-human
CC IL-1 antibody or is a mouse-human graft containing the CDR regions of
CC mouse anti-human IL-1 antibody,. The chimeric antibody is used to
CC treat diseases in which abnormal amounts of IL-1 are produced, eg.
CC inflammatory disease, arteriosclerosis, diffused intravascular
CC coagulation or leukemia. It can also be labelled and used for
CC diagnostic imaging of IL-1 producing sites in vivo.
SQ Sequence 129 AA;

Query Match 74.9%; Score 681; DB 9; Length 129;
Best Local Similarity 73.0%; Pred. No. 3.56e-42;
Matches 92; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

Db 1 msvptqvlglillwltardcdiqmtqpslsasvgrvtitcrtsqdimnlwnyqqtq 60
Qy 1 WYSSAQFLGLLLLCFQCTRCDIQMTQTTSLSASLGDRTVTISCRASQDISSYLNWYQKQ 60
Db 61 gkapklllytserlhsgvpsrfsgegsqtdyftisslqpediatyycqgktpwtfgq 120
Qy 61 DGTIKLLIYTSRLHSGVPSRFSGSGSDTYSLTINNLEQEDIATYFCQGGNTLPYTFGG 120
Db 121 gtlqi 126
Qy 121 GTKLEI 126

Search completed: Mon Jul 8 08:33:13 1996
Job time : 17 secs.

[illegible]

Result	Query			DB	ID	Description	Pred. No.
	No.	Score	Match Length				
1	835	83.3	149	5	S30752	Ig heavy chain precu	3.01e-89
2	828	82.6	135	5	P10100	Ig heavy chain precu	2.46e-88
3	774	77.2	134	5	B24672	Ig heavy chain precu	2.61e-81
4	768	76.6	116	2	HVMS1B	Ig heavy chain precu	1.57e-80
5	745	74.4	137	2	AVMS35	Ig heavy chain precu	1.51e-77
6	744	74.3	136	5	S07637	Ig heavy chain V reg	2.04e-77
7	736	73.5	119	11	C53285	monoclonal antibody	2.22e-76
8	729	72.8	117	11	I28195	Ig heavy chain V reg	1.79e-75
9	722	72.1	116	2	HVMS31	Ig heavy chain precu	1.44e-74
10	707	70.6	116	5	S38718	Ig heavy chain V reg	1.25e-72
11	673	67.2	115	11	S23932	Ig mu chain precursu	3.06e-68
12	672	67.1	106	5	S26464	Ig heavy chain V reg	4.11e-68

ALIGNMENTS

RESULT	1
ENTRY	
TITLE	S30752 #type complete
ORGANISM	Ig heavy chain precursor V region - mouse
DATE	#formal_name Mus musculus #common name house mouse 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1995
ACCESSIONS	S30752
REFERENCE	S30751
#authors	Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
#journal	Nucleic Acids Res. (1987) 15:5496
#title	Improved RNA sequencing method to determine immunoglobulin mRNA sequence.

ALIGNMENTS

```

1
RESULT
ENTRY
TITLE
ORGANISM
DATE
09-Sep-1995
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change

S30752 #type complete
Ig heavy chain precursor V region - mouse
#formal_name Mus musculus #common name house mouse
09-Sep-1995
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change

ACCESSIONS
REFERENCE
#authors
#journal
#title
Improved RNA sequencing method to determine immunoglobulin
mRNA sequence.
S30752
#accession
S30752
#molecule_type mRNA
#residues 1-149 #label GRA
#cross-references EMBL:X05878
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS
FEATURE
138-149
#domain C region (C-gamma 2b) (fragment) #status
predicted #label CRE
#length 149 #molecular-weight 16635 #checksum 9814
SUMMARY
Query Match 83.3%; Score 835; DB 5; Length 149;
Best Local Similarity 84.7%; Pred.No. 3.01e-89;
Matches 116; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

```

[illegible]

```

ENTRY
  TITLE      Ig heavy chain precursor V region (40-140) - mouse
  ORGANISM   Mus musculus #common name house mouse
  DATE       07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change
              12-Apr-1995

ACCESSIONS
  PL0100

REFERENCES
  PL0100
  Near, R.I.; Haber, E.
  Mol. Immunol. (1989) 26:371-382
  #authors
  #journal
  #title      Characterization of the heavy and light chain immunoglobulin
              variable region genes used in a set of anti-digoxin
              antibodies.
  #cross-references MWID:89238344
  #accession   PL0100
  ##molecule_type DNA
  ##residues    1-135 #label NEA
  ##experimental_source strain A/J
  ##note         the VH40-140 gene segment is classified as a member of
                  the 36-60 VH gene family

```

```

GENETICS
#introns
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
1-18
19-115
117-118
119-135
SUMMARY
#domain signal sequence #status predicted #label SIG\
#domain V segment #status predicted #label VRE\
#domain D segment #status predicted #label DRE\
#domain J segment #status predicted #label JRE
#length 135 #molecular-weight 15303 #checksum 9859
Query Match 82.6%; Score 828; DB 5; Length 135;
Best Local Similarity 84.7%; Pred. No. 2,46e-88;
Matches 116; Conservative 9; Mismatches 9; Indels 3; Gaps 2;

```

Db	1	mrvllllwlfafpgglsdvlqesggplkpsqslctetvtgysitsdyawsirafp	60
		: : : : : : : :	
Qy	1	MRVLLILLWLFAPPGILSDVOLQESGPVLKPSQSLSLCTVTGYSTSDHMSWIROFP	60
Db	61	gnrlewmgyityngtytnypelkerfsitrdsknqlflqlsvttedatyyvcarsyd-	119
Qy	61	GNRLEWMGYISYSGITTYNPSLKRSITRDTSKNQFFQLQNSVTTGDTSTYYCARSLAR	120
Db	120	-y-fdwagqgtltvas	134
		:	
Qy	121	TTAMDYWGQGTSTVTSVSS	137

RESULT	ENTRY	3
TITLE	B24672	#type complete
ORGANISM	Ig heavy chain precursor V region (VGM3-2)	- mouse mouse
	#formal name Mus musculus	#common name house mouse

```

DATE      19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change
          31-Dec-1993
ACCESSION B24672
REFERENCE  A91022
#authors  Winter, E.; Radbruch, A.; Krawinkel, U.
#journal  EMBO J. (1985) 4:2861-2867
#cross-references MUID:86055722
#accession B24672
#molecule_type DNA
#residues  1-134 #label WIN
#note      this sequence was determined from the differentiated
           gene

```

```

GENETICS
  15/1
#introns
CLASSIFICATION  #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
19-134          #product Ig heavy chain V region VGM3-2 #label VAT
                #length 134 #molecular-weight 15254 #checksum 6268
SUMMARY
Query Match      77.2%; Score 774; DB 5; Length 134;
Best local Similarity 82.5%; Pred. No. 2.61e-81;
Matches 113; Conservative 3; Mismatches 18; Indels 3; Gaps 2;

Db 1 mrவில்clftaagilsdvcloesqpdvlvkpsqslstctvgtifitgysvhwirqpf 60
Qy 1 MRVILLLELFTAPGLISDVLQIQESGPHVLRKPSQSLSUTCTVGTYSITDSHWIRQPF 60

Db 61 gnklewmyihyagstynvpelksrisitrdtsknofflqlnsvttedatycaryvd- 119
Qy 61 GNKLEWMYISYSGITTYNPSLAKSRISITRDTSKNOFFLQLNLSVTTGDTSTYYCARSLR 120

Db 120 -y-faywaggtlvtvsa 134
Qy 121 TTAMDYWGQGTSTVWS 137

```

RESULT	4
ENTRY	
TITLE	HVMS1B #type complete
ORGANISM	Ig heavy chain precursor V region (I43) - mouse
DATE	#formal_name Mus musculus #common name house mouse 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 18-Feb-1995
ACCESSIONS	JT0508
REFERENCE	JT0501
#authors	Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
#journal	J. Exp. Med. (1989) 169:2007-2019
#title	Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.

```

#molecule_type mRNA
#residues 1-116 #label LEV
#experimental_source strain BALB/cJ
#note amino acid sequence is not given
#note this sequence belongs to the VJ3660 subfamily
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE
1-18 #domain signal sequence #status predicted #label SIG
19-116 #product Ig heavy chain V region (IB43) #status
predicted #label MATV
33-116 #domain immunoglobulin homology #label IMM
#length 116 #molecule_weight 13158 #checksum 1197
SUMMARY

```

Jul 8 08:24

US-08-137-117B-31.rpr

5

```

Query Match          76.6%; Score 768; DB 2; Length 116;
Best Local Similarity 90.5%; Pred. No. 1.57e-80;
Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 1 mrvllllcftafgiledvqlqesopdlvlpqsgslctctvtgysitgyswhwirqfp 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 MRVLLLLWLTAFPGILSDVQLQESGPLVKPQSLSLTCTVTCTGYSITSDHAWSWIRQFP 60

Db 61 gnklemgyihyegntsympelksrtrdtsknfflqlnsvttedatyyccar 116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 GNKLEMGYISYSGITTYNPISKRSISITRDTSKNQFFLQLNSVTTGDTSTYYCAR 116

RESULT 5
ENTRY AVMS35 #type complete
TITLE Ig heavy chain precursor V region (MOPC 315) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE #sequence_revision 30-Jun-1992 #text_change 11-Aug-1995
ACCESSION PLO102; S03262; A93814; A91462; A93787
REFERENCE PLO102
#authors Rinfret, A.; Horne, C.; Dorrington, K.J.; Klein, M.
#journal Mol. Immunol. (1989) 26:431-434
#title Cloning, sequencing and expression of the rearranged MOPC 315
        VH gene segment.
#cross-references MUID:89238351
#accession PLO102
#molecule_type mRNA
#experimental_source strain MOPC 315
REFERENCE S03262
#authors Rinfret, A.; Dorrington, K.J.; Klein, M.
#submission submitted to the EMBL Data Library, June 1988
#accession S03262
#molecule_type DNA
#residues 1-15, 'G', 16-137 ##label R12
#cross-references EMBL:X07880
REFERENCE A93814
#authors Jilka, R.L.; Pestka, S.
#journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:5692-5696
#title Amino acid sequence of the precursor region of MOPC-315 mouse
        immunoglobulin heavy chain.
#cross-references MUID:78094475
#accession A93814
#molecule_type protein
#residues 1-14, 'H', 16-31 ##label J11
#note the authors translated mRNA in vitro to obtain the
        precursor protein
REFERENCE A91462
#authors Schechter, I.; Wolf, O.; Zemell, R.; Burstein, Y.
#journal Fed. Proc. (1979) 38:1839-1845
#title Structure and function of immunoglobulin genes and
        precursors.
#cross-references MUID:79148758
#accession A91462
#molecule_type protein
#residues 1, 'X', 3-11, 'X', 14-21 ##label SCH
#note the authors translated mRNA in vitro to obtain the
        precursor protein
REFERENCE A93787
#authors Francis, S.H.; Leslie, R.G.Q.; Hood, L.; Eisen, H.N.
#journal Proc. Natl. Acad. Sci. U.S.A. (1974) 71:1123-1127
#title Amino-acid sequence of the variable region of the heavy
        (alpha) chain of a mouse myeloma protein with anti-hapten
        activity.

```

Jul 8 08:24

US-08-137-117B-31.rpr

6

```

#cross-references MUID:74170779
#accession A93787
#molecule_type protein
#residues 19-52, 'K', 53-75, 'BYGB', 80-101, 'D', 103-106, 'ZB', 109-122,
        124-137 ##label FRA
REFERENCE A94484
#authors Hood, L.; Margolies, M.; Givol, D.; Zakut, R.
#citation unpublished results, cited by Padlan, E.A.; Davies, D.R.,
        Pecht, I., Givol, D., and Wright, C., Cold Spring Harbor
        Symp. Quant. Biol. 41, 627-637, 1977
#contents annotation; revision to residue 53
COMMENT This alpha chain was isolated from a myeloma protein that has
        anti-dinitrophenyl activity.

GENETICS
#introns 15/1
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
FEATURE
1-18 #domain signal sequence #status experimental #label SIG\
19-136 #product Ig heavy chain V region (MOPC 315) #label MAT\
33-116 #domain immunoglobulin homology #label IMM
SUMMARY #length 137 #molecular-weight 15399 #checksum 2186

Query Match          74.4%; Score 745; DB 2; Length 137;
Best Local Similarity 73.7%; Pred. No. 1.51e-71;
Matches 101; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Db 1 mkvllllylltaipgmsdvqlqesgplvlpqsgslctctvtgysitgyswhwirqfp 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 MRVLLLLWLTAFPGILSDVQLQESGPLVKPQSLSLTCTVTCTGYSITSDHAWSWIRQFP 60


Db 61 gnklewlgfikydngynpslknrvsitrdtsenqfflknsvttedatyyccagndh 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 GNKLEMGYISYSGITTYNPISKRSISITRDTSKNQFFLQLNSVTTGDTSTYYCARSLAR 120

Db 121 lyfydywgggtltvss 137
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 121 TTAMDYMQCGTSVTYSS 137

RESULT 6
ENTRY S07637 #type complete
TITLE Ig heavy chain V region (PTF.02) - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change
        28-Oct-1994
ACCESSION S07637
REFERENCE S07637
#authors Urakov, D.N.; Deev, S.M.; Polyanovsky, O.L.
#journal Nucleic Acids Res. (1989) 17:9481
#title The structure of the expressible VH gene from a hybridoma
        producing monoclonal antibodies against porcine
        transferrin.
#cross-references MUID:90067954
#accession S07637
#molecule_type DNA
#residues 1-136 ##label URA
#cross-references EMBL:X16740
#note the authors translated the codon TAT for residue 112 as
        Ile, TAC for residue 113 as Ile, and TAC for residue
        120 as Thr
GENETICS 15/3
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 136 #molecular-weight 15307 #checksum 182

```


(T1)



Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

```

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on:      Mon Jul  8 08:33:31 1996;  MasPar time 4.97 Seconds
           422.613 Million cell updates/sec

Tabular output not generated.

```

```
>US-08-137-117B-31
Title:
Description: (I-137) from US08137117B.pcp
Perfect Score: 1002
Sequence: 1 MRVLILLMLSTAFFGIGSDV.....LARTAMDYWGQCTSVTVSS 137
```

Scoring table: PAM 150
Gap 11

Searched: 43470 seas. 1535248 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database: swiss-prot31
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8
```

Statistics: Mean 42.978: Variance 84.975: scale 0.506

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		ID	Description	Pred. No.
		Match	Length			
1	768	76.6	116	HV61_MOUSE	IG HEAVY CHAIN PRECUR	2,01e-130
2	745	74.4	137	HV46_MOUSE	IG HEAVY CHAIN PRECUR	1,21e-125
3	722	72.1	116	HV60_MOUSE	IG HEAVY CHAIN PRECUR	7,13e-121
4	650	64.9	117	HV62_MOUSE	IG HEAVY CHAIN PRECUR	5,31e-106
5	609	60.8	113	HV47_MOUSE	IG HEAVY CHAIN V REGI	1,40e-97
6	499	49.8	144	HV43_MOUSE	IG HEAVY CHAIN PRECUR	3,32e-75
7	481	48.0	117	HV2G_HUMAN	IG HEAVY CHAIN V-II R	1,40e-71
8	481	48.0	135	HV02_XENLA	IG HEAVY CHAIN PRECUR	1,40e-71
9	469	46.8	146	HV21_HUMAN	IG HEAVY CHAIN PRECUR	3,59e-69
10	455	45.4	115	HV44_MOUSE	IG HEAVY CHAIN PRECUR	2,28e-66
11	442	44.1	116	HV45_MOUSE	IG HEAVY CHAIN PRECUR	8,99e-64
12	442	44.1	136	HV01_XENLA	IG HEAVY CHAIN PRECUR	8,99e-64
13	438	43.7	121	HV02_HUMAN	IG HEAVY CHAIN V-II R	5,64e-63

ALIGNMENTS

RESULT	1
ID	HV61 MOUSE STANDARD; PRT; 116 AA.
AC	P18532;
DT	01-NOV-1990 (REL. 16, CREATED)
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN PRECURSOR V REGION (1B43).
OS	MUS MUSCULUS (MUSEUR).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.
[1]	RN
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/CJ;
RM	89279149
RA	LEVY N.S., MALPIERO U.V., LEBECQUE S.G., GEARHART P.J.; J. EXP. MED. 169:2007-2019(1989).
RL	- THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
RR	PIR; J70508; HWS1B.
DR	HSP; F01825; 1BAF.
KW	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL 1 18
FT	CHAIN 19 116 IG HEAVY CHAIN V REGION (1B43). FRAMEWORK 1.
FT	DOMAIN 19 48
FT	DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
FT	DOMAIN 54 67
FT	DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2. FRAMEWORK 3.
FT	DOMAIN 85 116 BY SIMILARITY.
FT	DISULFID 40 114

AC	P01825;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
DE	IG HEAVY CHAIN V-II REGION (NEMM).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE.
RM	77242302
RA	POLJAK R.J., NAKASHIMA Y., CHEN B.L., KONIGSBERG W.;
RL	BIOCHEMISTRY 16:3412-3420(1977).
RN	[2]
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RM	78066916
RA	SAUL F.A., AMZEL L.M., POLJAK R.J.;
RL	J. BIOL. CHEM. 253:585-597(1978).
CC	-I- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
DR	PIR; A02100; GIHMN.
DR	PDB; /FAB; 3I-JAN-94.
KW	IMMUNOGLOBULIN V REGION; 3D-STRUCTURE.
FT	MOD_RES 1 1
FT	NON_TER 117 117
FT	STRAND 3 7
FT	TURN 11 12
FT	TURN 14 15
FT	STRAND 18 25
FT	TURN 30 31
FT	STRAND 33 39
FT	TURN 41 42
FT	STRAND 46 51
FT	TURN 53 54
FT	STRAND 57 59
FT	HELIX 61 63
FT	TURN 64 66
FT	STRAND 67 72
FT	TURN 73 76
FT	STRAND 77 82
FT	HELIX 87 89
FT	STRAND 91 98
FT	STRAND 104 107
FT	STRAND 111 115
SQ	SEQUENCE 117 AA; 12790 MW; 79791 CN;

Query Match	48.0%;	Score 481;	DB 4;	Length 117;
Best Local Similarity	54.6%;	Pred. No. 1.40e-71;		
Matches	65;	Conservative 29;	Mismatches 23;	Indels 2; Gaps 2;
Db	1	qvlegsgglvrpsdtlcltctwsgatfendy-ytwvrgpggrglewigvyfhgtsdd	59	
	:	:	:	:
	:	:	:	:
	:	:	:	:
QY	19	DVQLAESGVLVRPSQSLSLCTCTGVSTSDHAMSNIQFPCKNLEMGVYSYGITY	78	
Db	60	tptlrvtmldvtstkqfslrsvtadtavvyccarnli-agcidvwggqlvtvs	117	
	:	:	:	:
	:	:	:	:
	:	:	:	:
QY	79	NPSKRSISITROTCKNQFFQLNLNSVTGTDTYYCARSLARTAMDYQGGSVTVS	137	
RESULT	8			
ID	HV02_XENLA	STANDARD;	PRT;	135 AA.
AC	P20957;			
DT	01-FEB-1991	(REL. 17,	CREATED)	
DT	01-FEB-1991	(REL. 17,	LAST SEQUENCE UPDATE)	
DT	01-FEB-1991	(REL. 17,	LAST ANNOTATION UPDATE)	

```

DE IG HEAVY CHAIN PRECURSOR V REGION (XIG14) (FRAGMENT).
OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
NC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
RN
RC
RN
RM SEQUENCE FROM N.A.
RM 88176921
RA SCHWAGER J., MIKORYAK C.A., STEINER L.A.;
RL PROC. NATL. ACAD. SCI. U.S.A. 85:2245-2249(1988).
RL EMBL; J03632; XLIGHTB.
DR PTR; B31933; B31933.
DR HSSP; P01607; IFGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT NON TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 135 IG HEAVY CHAIN V REGION (XIG8).
FT NON TER 135 135
SQ SEQUENCE 135 AA; 15080 MW; 104336 CN;

Query Match 48.0%; Score 481; DB 4; Length 135;
Beat Local Similarity 52.2%; Pred. No. 1.40e-71;
Matches 71; Conservative 28; Mismatches 33; Indels 4; Gaps 4;

Db 2 fiiififfafspcilsqt-lqespgptvkpseelrltctvgfslsyhm-hwirqpgp 59
: : : : | | : | | : | | | | | | | | | | : | | | | |
Qy 4 LILLWLFAP-PG-IISDVLQESGPVLKVSQSLSLTCVTVGYSITSDHMSWIRQPPG 61
: : : : | | : | | : | | | | | | | | | | : | | | | |

Db 60 kglwlgviatggstaiadslnrvttikdngkqvylgmngmekvktamylcareyag 119
: | | : | : | : | : | | : | | : | | : | | : | | : | | | | |
Qy 62 NKLWMMGYISYSGITTPNSILKRSISITRDKNQFFLQINSVTTGDTSTYYCARSLART 121
: | | | | | | | | | | : | | : | | : | | : | | : | | | | |

Db 120 ynfdywgaggtmvtvs 135
: | | | | | | | | | | : | | : | | : | | : | | : | | | | |
Qy 122 TAMDYWGOGTSTVWSS 137
: | | | | | | | | | | : | | : | | : | | : | | : | | | | |

```

RESULT	9	STANDARD;	PRT;	146 AA.
ID	HV21 HUMAN			
AC	P06331;			
DT	01-JAN-1988 (REL. 06, CREATED)			
DT	01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)			
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN PRECURSOR V-II REGION (ARIH-77).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RM	85205332			
RA	KUDO A., ISHIHARA T., NISHIMURA Y., WATANABE T.;			
RL	GENE 33:181-189(1985).			
DR	PIR; A02101; GI4UH2.			
DR	HSP; P01825; IFGV.			
KW	IMMUNOGLOBULIN V REGION; SIGNAL.			
FT	SIGNAL	1	19	
FT	CHAIN	20	146	
FT	DOMAIN	20	117	
FT	DOMAIN	118	127	
FT	DOMAIN	128	146	
FT	DISULFID	42	115	
FT	NON TER	146	146	
SQ	SEQUENCE	146 AA;	16228 MW;	127884 CN;
Query Match		46.8%;	Score 469;	DB 4;
Best Local Similarity		55.9%;	Pred. No. 3,59e-69;	Length 146;

Jul 8 08:23

US-08-137-117B-31.rsp

9

Matches 80; Conservative 24; Mismatches 28; Indels 11; Gaps 5;
 Db 6 flllwcqldv-gvleqvlqwgaglvkpaetlsitcavfigsf-sgyvswirgppqr 63
 :||| : |||:||||: : |||:||||:||||:| : | ||||| ||
 Qy 4 LILLM-LTAFPGILSDVQLQESGVLVWKPQSLSLCTCTVTCYSITSDHMSWIRQFPGN 62
 64 glwigeinhagstnyktelkarvtlaidteknlfelklsavtaadtavyycargllrsg 123
 ||||:| : || : |||:||||: ||||| | : |||:||||: |||||:|
 Qy 63 KLEWGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTTYCARSLART- 121
 124 wncdvdyvvgmdvqgqgtvtvss 146
 :|| |||:|||||
 Qy 122 -TAMDY-----WGQGTSTVTSS 137

RESULT 10
 ID HV44 MOUSE STANDARD; PRT; 115 AA.
 AC P01870;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (PJ14).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 81012133
 RA SAKANO H., MAKI R., KUROSAWA Y., ROEDER W., TONEGAWA S.;
 RL NATURE 286:676-683(1980).
 DR PIR; A02095; HWS14.
 DR HSP; P01772; IFDL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 115 IG HEAVY CHAIN V REGION (PJ14).
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12447 MW; 73384 CN;

Query Match 45.4%; Score 455; DB 4; Length 115;
 Best Local Similarity 57.8%; Pred. No. 2,28e-66;
 Matches 67; Conservative 23; Mismatches 24; Indels 2; Gaps 2;
 Db 1 mavlllclvtlfpccilseqvqlkspqvlvapeqslitctvsgfcltg-ygvnwvrgp 59
 | ||| : : || : |||:|||| || ||||| || |||||:||||:| : : |||||
 Qy 1 MRVLILLMLTAFPG-ILSDVQLQESGVLVWKPQSLSLCTCTVTCYSITSDHMSWIRQF 59
 60 pkgglewlgmldgtdynaalkslslskdsksqvflkmlslqtdtdtaryyca 115
 ||: ||||:| | | |||:||||:||||: |||: || : |||: |||: |||||
 Qy 60 PGNKLEWGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTTYCA 115

RESULT 11
 ID HV45 MOUSE STANDARD; PRT; 116 AA.
 AC P01871;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (MC101).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 82075900

Jul 8 08:23

US-08-137-117B-31.rsp

10

RA KATAOKA T., NIKAIKO T., MIYATA T., MORIWAKI K., HONJO T.;
 RL J. BIOL. CHEM. 257:277-285(1982).
 DR PIR; A02096; GIMS10.
 DR HSP; P01772; IFDL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 116 IG HEAVY CHAIN V REGION (MC101).
 FT NON TER 116 116
 SQ SEQUENCE 116 AA; 12593 MW; 75942 CN;

Query Match 44.1%; Score 442; DB 4; Length 116;
 Best Local Similarity 53.8%; Pred. No. 8,99e-64;
 Matches 63; Conservative 27; Mismatches 25; Indels 2; Gaps 2;
 Db 1 mavlgllfclvtfpccilseqvqlkspqvlvapeqslitctvsgfcltg-ygvnwvrgp 59
 | ||| : : || : |||:|||| || ||||| || |||||:||||:| : |||||
 Qy 1 MRVLILLMLTAFPG-ILSDVQLQESGVLVWKPQSLSLCTCTVTCYSITSDHMSWIRQF 59
 60 pkgglewlgmldgtdynaalkslslskdsksqvflkmlslqtdtdtaryyca 116
 ||: ||||:| | | |||:||||:||||: |||: || : |||: |||: |||||
 Qy 60 PGNKLEWGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTTYCAR 116

RESULT 12
 ID HV01 XENLA STANDARD; PRT; 136 AA.
 AC P20956;
 DT 01-FEB-1991 (REL. 17, CREATED)
 DT 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
 DT 01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (XIG8) (FRAGMENT).
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RM 88176921
 RA SCHWAGER J., MIKORYAK C.A., STEINER L.A.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 85:2245-2249(1988).
 DR EXBL; M20484; XLIGHA.
 DR PIR; A31933; A31933.
 DR HSP; P01789; 2FGW.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT NON TER 1 1
 FT SIGNAL <1 18
 FT CHAIN 19 136 IG HEAVY CHAIN V REGION (XIG8).
 FT NON TER 136 136
 SQ SEQUENCE 136 AA; 15123 MW; 110289 CN;

Query Match 44.1%; Score 442; DB 4; Length 136;
 Best Local Similarity 47.4%; Pred. No. 8,99e-64;
 Matches 64; Conservative 33; Mismatches 35; Indels 3; Gaps 3;
 Db 4 ifvifmffscilseqt-lqesgqvtvkpselrlitctvsgfcltg-yvwrpqr 61
 :||| : : |||: ||||| |||||:||||: ||||| : |||||
 Qy 4 LILLMLTAFPGILSDVQLQESGVLVWKPQSLSLCTCTVTCYSITSDHMSWIRQFPGNK 63
 62 lewigvrtgdstaidelknrvtkdngkqvlmgmvevkdtdamyyctatlagtag 121
 ||||:| : | : |||:||||:| : |||:||||: |||: |||: |||||
 Qy 64 LEWGYISYSGITTYNPSIKSRISITRDTSKNQFFLQINSVTTGDTSTTYCARSLART 123
 122 yfhwgqgtmvtvs 136
 : ||||| |||||
 Qy 124 -MDYWGQGTSTVTSS 137

Jul 8 08:23

US-08-137-117B-31.rsp

13

Search completed: Mon Jul 8 08:34:03 1996
Job time : 32 secs.

(T)

1. 2. 3. 4. 5. 6.

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.

MPPerch pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jul 8 08:34:49 1996; MasPar time 4.28 Seconds
265.081 Million cell updates/sec

Tabular output not generated.

```

Title:
Description: (1-137) from US08137117B.pap
Perfect Score: 1002
Sequence: 1 MRVLILLMLFAPFGILSDV.....LARTTAMDYWGQGTSTVTVSS 137

```

Scoring table: PAM 150
Gap 11

Searched: 70887 seqs, 8282111 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:
a-geneseq22
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14

Statistics: Mean 30.530; Variance 155.534; scale 0.196

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB ID	Description	Pred. No.	
	Score	Match	Length				
1	1002	100.0	137	6	R28671	pPM-hl protein produc	6.61e-72
2	747	74.6	138	6	R29014	pUC-RVh-PM1f-4.	8.43e-51
3	747	74.6	138	6	R29012	pUC-RVh-PM1f.	8.43e-51
4	726	72.5	240	7	R34510	Fv(TU27).	4.52e-49
5	721	72.0	130	6	R33308	MaE13 heavy chain.	1.16e-48
6	704	70.3	126	5	R24722	Sequence encoded by t	2.91e-47
7	686	68.5	122	5	R24721	Sequence of a chimeri	8.77e-46
8	664	66.3	114	9	R48617	Sequence of the monoc	5.60e-44
9	664	66.3	117	2	R07318	VH domain of antibody	5.60e-44
10	656	65.5	225	12	R63118	Heavy chain of 58.2 a	2.54e-43
11	615	61.4	134	6	R33306	MaE11 heavy chain.	5.76e-40
12	611	61.0	113	7	R38608	HYH heavy chain.	1.22e-39

13	606	60.5	137	6	R33310	MAE15 heavy chain.	3.13e-39
14	596	59.5	909	10	R50092	Humanised anti-CEA sF	2.06e-38
15	589	58.8	240	1	P080157	BioSynthetic antibody	7.66e-38
16	582	58.1	134	6	R33345	Sequence of the varia	2.85e-37
17	576	57.5	134	8	R40613	Sequence of the monoc	8.80e-37
18	572	57.1	117	8	R40953	Human germ-line gene	1.86e-36
19	572	57.1	119	6	R30143	MAB GAH variable regi	1.86e-36
20	569	56.8	121	13	R65171	Murine NN-01 variable	3.27e-36
21	569	56.8	121	9	R486114	Sequence of the monoc	3.27e-36
22	567	56.6	121	13	R651173	Region for producing	4.76e-36
23	545	54.4	118	5	R29701	431/26 VH hum.	2.94e-34
24	542	54.1	120	9	R48621	Sequence of the human	5.16e-34
25	534	53.3	117	12	R66320	Human immunoglobulin	2.30e-33
26	533	53.2	142	7	R13285	F105 rearranged varia	2.78e-33
27	533	53.2	144	10	R53344	NEWB human Ab H chain	2.78e-33
28	531	53.0	135	2	P70991	Sequence of the heavy	4.04e-33
29	529	52.8	117	7	R38669	Ab26.	5.87e-33
30	527	52.6	141	6	R31948	Anti-CD4 VH peptide.	8.53e-33
31	526	52.5	118	12	R66322	Human immunoglobulin	1.03e-32
32	523	52.2	116	12	R66346	Human immunoglobulin	1.80e-32
33	523	52.2	116	7	R42689	Human immunoglobulin	1.80e-32
34	523	52.2	118	12	R66348	Human immunoglobulin	1.80e-32
35	520	51.9	124	2	R12266	Anti-human RhD PAG-1	3.15e-32
36	516	51.5	220	12	R74782	Heavy chain of 59.1 a	6.66e-32
37	513	51.2	122	6	R30145	MAB 1-3-1 variable re	1.17e-31
38	511	51.0	470	4	R23257	Reshaped CAMPATH-1 an	1.69e-31
39	509	50.8	183	6	R32128	Anti-IL2R-alpha antib	2.46e-31
40	509	50.8	183	3	R15326	IL-2 chimeric antibod	2.46e-31
41	507	50.6	111	4	R625714	Heavy chain VH14.1 fr	3.57e-31
42	507	50.6	114	12	R22919	Human cytomegalovirus	3.57e-31
43	507	50.6	120	10	R54929	Fc receptor humanized	3.57e-31
44	506	50.5	144	1	P80892	V region of H chain o	4.30e-31
45	504	50.3	242	2	R06483	18-2-3-7/TRY59.	6.25e-31

ALIGNMENTS

RESULT	1	
ID	R28671 standard; Protein; 137 AA.	
AC	R28671;	
DT	30-MAR-1993 (first entry)	
DE	pPM-h1 protein product.	
KW	Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H; heavy chain; variable region; mouse; monoclonal; hybridoma; PM1; plasmid; pPM-k3; pPM-h1.	
OS	Synthetic.	
Key	Location/Qualifiers	
FT	Peptide 1..18	
FT	/note= "Signal peptide"	
FT	Protein 19..137	
FT	/note= "Mature peptide"	
PN	W09219759-A.	
PD	12-NOV-1992.	
PF	24-APR-1992; J00544.	
PR	25-APR-1991; JP-095476.	
PR	19-FEB-1992; JP-032084.	
PA	(CHUS) CHUGAI SEIYAKU KK.	
PI	Bendig MM, Jones ST, Saldanha JW, Sato K, Tsuchiya M;	
DR	WPI; 92-398882/48.	
DR	N-PSDB; Q30756.	
PT	Reconstituted human antibody to human interleukin-6 receptor -	
PT	has low antigenicity and contains mouse V-region complementarity	
PS	determining regions	
PS	Disclosure; Page 122-123; 207pp; Japanese.	

Jul 8:08:24

US-08-137-117B-31.rag

5

PS Disclosure; Page 138-9; 207pp; Japanese.
CC The sequences given in R29012-15 are portions of monoclonal antibodies
CC which were encoded by plasmids derived from mouse hybridomas. The DNA
CC encoding complementarity determining regions (CDR's) was isolated by
CC polymerase chain reaction. These antibodies recognise human
CC interleukin-6 receptor (IL-6R). The mouse hybridoma cells were
CC transformed with the plasmids encoding these genes which caused the
CC secretion of these antibodies from the hybridoma cells.
SQ Sequence 138 AA;

Query Match 74.6%; Score 747; DB 6; Length 138;
Best Local Similarity 75.9%; Pred. No. 8.43e-51;
Matches 101; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

Db 6 illflvatgshvqqlqesgplvrpqtclctvsgysitshawsrqpgrgl 65
QY 5 ILLWLTAFPCILLSDVQLQESGPVLPKPSQSLSTCTVTGYSITSDHAWSWIRQFGNKL 64
Db 66 ewigvisgittynpslksrvtmldtsknqfslrsvtaadtavycarslarttam 125
QY 65 EWGVISYSGITTYNPSLKSRSITSDTSKNQFFLQLNSVTGDTSTYYCARSARTTAM 124
Db 126 dywggsglvtvss 138
QY 125 DYWGQGSTVTSS 137

RESULT 4

ID R34510 standard; Protein; 240 AA.
AC R34510;
DT 20-AUG-1993 (first entry)
DE Fv(TU27).
KW pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;
KW heavy; beta; chain; interleukin; IL-2; receptor; inhibition;
KW immunomodulator; immunosuppressant; graft rejection; allergy;
KW autoimmune disease; leukemia; cyclosporin.
OS Homo sapiens.
PN EP-539748-A.
PF 05-MAY-1993.
PD 30-SEP-1992; 116746.
PR 03-OCT-1991; JP-256335.
PA (AJIN) AJINOMOTO KK.
PI Hamuro J, Shimamura T, Taki S;
DR WPI; 93-145163/18.
DR N-PSDB; Q40462.
PT Polypeptide(s) which bind H chain of human IL-2 receptors - for
PT treating inflammatory, allergic and auto-immune disorders,
PT leukaemias etc.
PS Claim 3; Page 18; 27pp; English.
CC The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express
CC polypeptides consisting only of the V regions were purified and
CC sequenced. The polypeptides are capable of binding to the beta
CC chain of IL-2 receptor and of inhibiting the binding of IL-2 to the
CC receptor. They are useful as immunomodulators and
CC immunosuppressants, e.g. to prevent graft rejection or to treat
CC inflammatory allergic and autoimmune diseases, or leukemia. Unlike
CC cyclosporin etc. they are both effective and safe.
SQ Sequence 240 AA;

Query Match 72.5%; Score 726; DB 7; Length 240;
Best Local Similarity 82.5%; Pred. No. 4.52e-49;
Matches 99; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

Db 122 tqvkleesgplvkvpsqltctvtgypitsdyawdirfpqgnklewmgyvsgstd 181

Jul 8:08:24

US-08-137-117B-31.rag

6

QY 18 SDVQLQESGPVLVPKPSQSLSTCTVTGYSITSDHAWSWIRQFGNKLWGYISGITT 77
Db 182 ypslkerisrdsrtdsknqfflqlnsvttedatyycarg-gfpyamydywgqgtvtvss 240
QY 78 YNPSLKSRISITRDTSKNQFFLQLNSVTGDTSTYYCARSARTTAMDYWGQGSTVTSS 137

RESULT 5

ID R33308 standard; protein; 130 AA.
AC R33308;
DT 05-JUL-1993 (first entry)
DE MAE13 heavy chain.
KW Antibody; high affinity; FCEH; low affinity; FCEL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; MAE13; MAE15; MAE17.
OS Synthetic.
PN MO9304173-A.
PD 04-MAR-1993.
PF 14-AUG-1992; U06860.
PR 14-AUG-1991; US-744768.
PR 07-MAY-1992; US-879495.
PA (GETH) GENENTECH INC.
PI Jardieu PM, Presta LG;
DR WPI; 93-094004/11.
PT Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
PS Disclosure; Fig 2; 113pp; English.
CC Antibodies capable of binding FCEL-bound IgE but which are
CC substantially incapable of binding FCEH-bound IgE or inducing
CC histamine release from mast cells or basophils, comprise a human
CC Kabat CDR domain into which has been substituted a positionally
CC analogous residue from a Kabat CDR domain of the murine anti-huIgE
CC antibodies MAE11, MAE13, MAE15 or MAE17.
SQ Sequence 130 AA;

Query Match 72.0%; Score 721; DB 6; Length 130;
Best Local Similarity 85.7%; Pred. No. 1.16e-48;
Matches 102; Conservative 8; Mismatches 7; Indels 2; Gaps 1;

Db 1 dvqlqesgplvlpesqltctvtgysitshawsrqpqgnklewmgyinhggttsy 60
QY 19 DVQLQESGPVLVPKPSQSLSTCTVTGYSITSDHAWSWIRQFGNKLWGYISGITT 78
Db 61 npslkerisrdsrtdsknqfflqlnsvttedatyycawvva--yamydywgqgtvtvss 117
QY 79 NPSLKSRISITRDTSKNQFFLQLNSVTGDTSTYYCARSARTTAMDYWGQGSTVTSS 137

RESULT 6

ID R24722 standard; Protein; 126 AA.
AC R24722;
DT 28-DEC-1992 (first entry)
DE Sequence encoded by the anti-urokinase antibody kappa variable region
DE (VK) cDNA
KW Chimeric monoclonal antibody; anti-urokinase antibody; PCR;
KW antithrombotic agent; myocardial infarction therapy.
OS Mus musculus.
FH Key Location/Qualifiers
FT Region 34..39
FT /label= complementarity determining region (CDR)1
FT Region 54..69
FT /label= CDR 2

FT Region 102...113
 FT /label= CDR 3
 PN EP-491351-A.
 PD 24-JUN-1992.
 PF 17-DEC-1991; 121591.
 PR 18-DEC-1990; JP-413829.
 PA 11-NOV-1991; JP-294464.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Iwasa S, Taka H, Watanabe T, Tada H;
 DR WPI; 92-209528/26.
 DR N-PSDP; Q25667.
 PT Chimeric monoclonal antibodies - contain anti-human fibrin
 PT antibody light and heavy chain variable and constant for treating
 PT thrombotic conditions e.g. myocardial infarction
 PS Example; Figure 15; 87pp; English.
 CC Poly(A)+ RNA was prep'd. from mouse anti-urokinase
 CC antibody-producing hybridoma UK1-3 cells. Using this poly(A) RNA as
 CC a template, an anti-urokinase antibody VK cDNA was amplified with
 CC the mC-kappa primer as primer for first strand synthesis, and the
 CC 3'mV-kappa and 5'mV-kappa primers as primers for the PCR. The
 CC amplified fragment was restriction digested and ligated into a
 CC restriction fragment of pTB1423 to give an anti-urokinase antibody
 CC VK cDNA contg. plasmid pTB1456. The sequence of this plasmid is
 CC given in Q25667. The cDNA is a functional VK gene. The sequence of
 CC the primer (mC-gamma-1) is given in Q25689.
 SQ Sequence 126 AA;

Query Match 70.3%; Score 704; DB 5; Length 126;
 Best Local Similarity 81.0%; Pred. No. 2.91e-47;
 Matches 98; Conservative 10; Mismatches 11; Indels 2; Gaps 2;
 Db 4 evqlvespgqlvkpsqslctctvtsitedatycarlqgfdagdyfdywgqgttvtvs 123
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 19 DVQLQESGPVLVWPQSLSLCTCTVTCVTSITSDHAWSWIRQFPGNKLEWNGYISYGITY 78
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 64 npslksrisitrdtnnqfflqlnsvtsedatycarlqgfdagdyfdywgqgttvtvs 123
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 79 NPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCAR-S-LARTTAMDYWGQGTSTVTS 136

Db 124 s 124
 QY 137 S 137

RESULT 7
 ID R24721 standard; Protein; 122 AA.
 AC R24721;
 DT 28-DEC-1992 (first entry)
 DE Sequence of a chimeric urokinase-recognising antibody heavy chain
 DE variable region contg. complementarity determining regions (CDRs)
 DE J, K and L.
 KW Chimeric monoclonal antibody; anti-urokinase antibody;
 KW antithrombotic agent; myocardial infarction therapy.
 OS Synthetic.
 FS Key Location/Qualifiers
 FT Region 31...36
 FT /label= CDR J
 FT Region 51..66
 FT /label= CDR K
 FT Region 99..110
 FT /label= CDR L
 PN EP-491351-A.
 PD 24-JUN-1992.
 PF 17-DEC-1991; 121591.

PR 18-DEC-1990; JP-413829.
 PR 11-NOV-1991; JP-294464.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Iwasa S, Taka H, Watanabe T, Tada H;
 DR WPI; 92-209528/26.
 PT Chimeric monoclonal antibodies - contain anti-human fibrin
 PT antibody light and heavy chain variable and constant for treating
 PT thrombotic conditions e.g. myocardial infarction
 PS Disclosure; Page 10; 87pp; English.
 CC The inventors claim a chimeric monoclonal antibody which contains a
 CC urokinase-recognising antibody heavy chain variable region contg. at
 CC least one of the polypeptide chains J, K and L (R24717, R24718, R24719)
 CC and a human antibody heavy chain constant region. A pref'd. chimeric
 CC monoclonal antibody contains all three complementarity determining
 CC regions. The chimeric Abs can be used both in vivo and in vitro
 CC and, since they have very low immunogenicity as compared with mouse
 CC Abs, they can be administered to humans for diagnostic and
 CC therapeutic purposes. They are also more stable and show a longer
 CC half-life in the blood as compared with the original mouse Abs.
 SQ Sequence 122 AA;

Query Match 68.5%; Score 686; DB 5; Length 122;
 Best Local Similarity 80.2%; Pred. No. 8.77e-46;
 Matches 97; Conservative 10; Mismatches 11; Indels 3; Gaps 3;
 Db 1 evqlvespgqlvkpsqslctctvtsitedatycarlqgfdagdyfdywgqgttvtvs 59
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 19 DVQLQESGPVLVWPQSLSLCTCTVTCVTSITSDHAWSWIRQFPGNKLEWNGYISYGITY 78
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 60 npslksrisitrdtnnqfflqlnsvtsedatycarlqgfdagdyfdywgqgttvtvs 119
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 QY 79 NPSLKSRISTRDTSKNQFFLQLNSVTGDTSTYYCAR-S-LARTTAMDYWGQGTSTVTS 136
 :||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 120 s 120
 QY 137 S 137

RESULT 8
 ID R48617 standard; Protein; 114 AA.
 AC R48617;
 DT 03-SEP-1994 (first entry)
 DE Sequence of the monoclonal antibody BAT123 heavy chain
 DE variable region.
 KW Epitope; monoclonal antibody; BAT123; variable heavy.
 OS Synthetic.
 PN W09404574-A.
 PD 03-MAR-1994.
 PF 24-AUG-1993; U07967.
 PR 24-AUG-1992; WO-007111.
 PR 22-APR-1993; US-039457.
 PA (NISP) NISSIN SHOKUIN KAISHA LTD.
 PI Ohno T;
 DR WPI; 94-083117/10.
 PT New humanised antibody specific for epitope on HIV-1 gp 120 -
 PT able to neutralise infection of HG cells, also nucleic acid
 PT encoding it, useful for passive immunisation to treat or prevent
 PT HIV-1 infection
 PS Example; Page 46-47; 91pp; English.
 CC GPCR is a portion of HIV-1 gp120 or gp160 protein. Monoclonal
 CC antibodies (MAbs) that react with this and which have the capacity
 CC to neutralise the infection of H9 cells in culture by live HIV-1
 CC strains MN and IIIB are claimed. Specifically illustrating the
 CC invention are the murine MAbs (designated NM-01) produced by

Jul 8 08:24

US-08-137-117B-31.rag

9

CC hubridoma cell line HB 10726 which is deposited under ATCC No. HB
CC 10726. The DNA sequences of the variable regions of the heavy and
CC light chains of Mab NM-01 were cloned by PCR using cDNA generated
CC from hybridoma HB 10726 cytoplasmic RNA as template. The DNA was
CC then sequenced. The DNA and deduced AA sequences are given in
CC Q56685/R48613; Q56686/R48615. Resequencing the variable regions
CC of Mab NM-01 resulted in the sequences set out in Q56687/R48614
CC and Q56688/R48616. The heavy chain variable region of NM-01
CC differs from that of the Mab BA123, as reported in Liou et al.,
CC by 46 AAs out of a total of 120. The light chain variable regions
CC of these two Abs differ by 23 AAs. Significantly, the three CDRs
CC in the heavy chain (V-H) of the NM-01 molecule are about 41 to 90%
CC different in sequence from those of BA123, while the sequences of
CC the three CDRs in the light chain (V-L) vary by about 29-47%
CC compared to NM-01.
SQ Sequence 114 AA;

Query Match 66.3%; Score 664; DB 9; Length 114;
Best Local Similarity 82.4%; Pred. No. 5,60e-44;
Matches 98; Conservative 9; Mismatches 7; Indels 5; Gaps 3;

Db 1 evqlqesgdlvlpqsglslelctvtgysitdsydwawwirqfpgnklemgysygetty 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 19 DVQLQESGPVLVLPKPSQSLSLTCTVTCYSITSDHAWSWIRQPPGNKLEWNGYISYGITTY 78

Db 61 npslkerisrtdsknflqlasvtaedtatyccary---sfg-d-wgqgtlvtvsa 114
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 79 NPSLKRISITRDTSKNQFFLQLNSVTTGDTSTYYCARSILARTTANDYWGQGTSTVTSS 137

RESULT 9

ID R07318 standard; protein; 117 AA.
AC R07318;
DT 22-JAN-1991 (first entry)
DE VH domain of antibody B against tumour-associated antigens.
KW Tumour-associated antigen; murine monoclonal antibody B;
KW gastrointestinal carcinoma; ovary; pulmonary adenocarcinoma;
KW diagnosis.
OS Mus musculus.
PN EP-388914-A.
PD 26-SEP-1990.
PF 21-MAR-1990; 105322.
PR 24-MAR-1989; DE-909799.
PA (BEHW) BEHRINGWERKE AG.
PI Bosslet K, Seemann G, Sedlacek HH;
DR WPI; 90-291873/39.
DR N-PSDB; Q07318.
PT Monoclonal antibodies to tumour associated antigens - used for
PT diagnosis of malignant tumours etc.
PS Disclosure; Page 12; 18pp; German.
CC Antibody B is produced as described in EP-141079 and binds to cells
CC almost all gastrointestinal carcinomas and to certain ovary
CC carcinomas and pulmonary adenocarcinomas.
CC They are useful in tumour diagnosis and therapy.
CC See also Q06215 for VK of Mab B, Q07312-13 for Mab A and Q06227-30
CC for Mab C and D.
SQ Sequence 117 AA;

Query Match 66.3%; Score 664; DB 2; Length 117;
Best Local Similarity 82.1%; Pred. No. 5,60e-44;
Matches 96; Conservative 3; Mismatches 17; Indels 1; Gaps 1;

Db 1 lqesgdlvlpqsglslelctvtgysitdsydwawwirqfpgnklemgysygetty 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

Jul 8 08:24

US-08-137-117B-31.rag

10

Qy 22 LQESGPVLVLPKPSQSLSLTCTVTCYSITSDHAWSWIRQPPGNKLEWNGYISYGITTYPS 81

Db 61 lkerisrtdsknflqlasvtaedtatyccaredydhwyfdwaggtvtvsa 117
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 82 LKSRISITRDTSKNQFFLQLNSVTTGDTSTYYCAR-SLARTTANDYWGQGTSTVTSS 137

RESULT 10

ID R63118 standard; peptide; 225 AA.
AC R63118;
DT 26-JUN-1995 (first entry)
DE Heavy chain of 58.2 an anti-HIV antibody.
KW Identifying compounds; anti-HIV antibodies; HIV treatment;
KW peptide AS; antibody 58.2.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified site 160
FT /label= OTHER
FT /note= "CPR no further definition"
FT Modified site 162
FT /label= OTHER
FT /note= "CPR no further definition"
FT Modified site 201
FT /label= OTHER
FT /note= "CPR no further definition"
FT Modified site 201
FT /label= OTHER
FT /note= "CPR no further definition"
PN W09418232-A.
PD 18-AUG-1994.
PF 09-FEB-1994; U01458.
PR 12-FEB-1993; US-017485.
PA (REPK) REPLIGEN CORP.
PA (SCRI) SCRIPPS RES INST.
PI Profy AT, Wilson IA;
DR WPI; 94-332662/41.
PT Identifying cpds. which elicit, or bind to, anti-HIV antibodies -
PT and new antibodies which neutralise a broad range of HIV strains
PS Disclosure; Page 50; 137pp; English.
CC R63118 describes the amino acid sequence of the heavy chain of
CC 58.2 an anti-HIV antibody (Ab), it was used in the development of
CC the peptide AS (R63119). This peptide can bind to anti-HIV Abs or
CC elicit new Abs effective against a broad range of HIV strains,
CC that can be used in the treatment of HIV infection.
SQ Sequence 225 AA;

Query Match 65.5%; Score 656; DB 12; Length 225;
Best Local Similarity 78.6%; Pred. No. 2,54e-43;
Matches 99; Conservative 10; Mismatches 10; Indels 7; Gaps 3;

Db 1 dvqlqesgdlvlpqsglslelctvtgysitdsydwawwirqfpgnklemgysygetty 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 19 DVQLQESGPVLVLPKPSQSLSLTCTVTCYSITSDHAWSWIRQPPGNKLEWNGYISYGITTY 78

Db 61 npslkerisrtdsknflqlasvtaedtatyccareampygnqayyyandwgggt 120
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy 79 NPSLKRISITRDTSKNQFFLQLNSVTTGDTSTYYCAR-SLA---RTT---AMDYWGQGT 131
121 tvttvas 126
:|||||
Qy 132 SVTVSS 137

RESULT 11

ID R33306 standard; protein; 134 AA.
AC R33306;
DT 05-JUL-1993 (first entry)

* * * * *
 FILE 'USPAT' ENTERED AT 10:35:38 ON 03 JUL 96
 * * * * *
 * W E L C O M E T O T H E *
 * U . S . P A T E N T T E X T F I L E *
 * * * * *

=> s human interleukin 6 receptor?

133546 HUMAN
 2317 INTERLEUKIN
 1835874 6

23249 RECEPTOR?

L1 3 HUMAN INTERLEUKIN 6 RECEPTOR?
 (HUMAN(W) INTERLEUKIN(W) 6(W) RECEPTOR?)

=> d 1-3 bib ab clm

US PAT NO: 5,447,851 [IMAGE AVAILABLE] L1: 1 of 3
 DATE ISSUED: Sep. 5, 1995
 TITLE: DNA encoding a chimeric polypeptide comprising the
 extracellular domain of TNF receptor fused to IgG,
 vectors, and host cells
 INVENTOR: Bruce A. Beutler, Dallas, TX
 Karsten Poppel, Dallas, TX
 David F. Crawford, Irving, TX
 ASSIGNEE: Board of Regents, The University of Texas System, Austin,
 TX (U.S. corp.)
 APPL-NO: 07/862,495
 DATE FILED: Apr. 2, 1992
 ART-UNIT: 182
 PRIM-EXMR: Garnette D. Draper
 ASST-EXMR: K. Cochrane Carlson
 LEGAL-REP: Arnold, White & Durkee

US PAT NO: 5,447,851 [IMAGE AVAILABLE] L1: 1 of 3

ABSTRACT:

The invention relates generally to DNA sequences encoding chimeric polypeptides comprising extracellular portions of cytokine receptor polypeptides attached to a sequence encoding portions of IgG polypeptides. The invention relates generally, as well, to DNA sequences encoding chimeric polypeptides comprising extracellular portions of cytokine receptor polypeptides attached through oligomers encoding specifically cleavable peptide linkers to a sequence encoding portions of IgG heavy chain polypeptides. More specifically, the invention relates to a construction in which a cDNA sequence encoding the extracellular domain of the human 55 kD TNF receptor is attached through an oligomer encoding a thrombin-sensitive peptide linker to a sequence encoding the F.sub.c portion and hinge region of a mouse IgG1 heavy chain. The invention relates as well to uses of the chimeric polypeptide, including: use as a reagent for the antagonism and assay of TNF and lymphotoxin from diverse species; use as a means of determining the mechanism by which TNF, or analogs thereof, interacts with the TNF receptor; use as an antitumor reagent, particularly against placental tumors; and, use as a reagent capable of controlling birth.

CLAIMS:

CLMS(1)

What is claimed is:

1. An isolated DNA segment having a sequence encoding a chimeric polypeptide comprising the extracellular domain of a TNF receptor polypeptide functionally attached to a Fc portion and hinge region of an IgG heavy chain polypeptide.

CLMS(2)

2. The isolated DNA segment of claim 1, where the TNF receptor polypeptide is a human TNF receptor polypeptide.

CLMS(3)

3. The isolated DNA segment of claim 1, where the IgG heavy chain polypeptide is a mouse IgG polypeptide.

CLMS(4)

4. The isolated DNA segment of claim 1, further incorporating a DNA segment encoding a specifically cleavable linker peptide functionally interposed between the TNF receptor polypeptide and the Fc portion.

CLMS(5)

5. The isolated DNA segment of claim 4, where the specifically cleavable linker peptide comprises a thrombin-sensitive linker peptide.

CLMS(6)

6. A recombinant vector incorporating a DNA segment as defined by claim 1.

CLMS(7)

7. The recombinant vector of claim 6, where the TNF receptor polypeptide is a human TNF receptor polypeptide.

CLMS(8)

8. The vector of claim 6, where the IgG heavy chain polypeptide is a mouse IgG polypeptide.

CLMS(9)

9. The vector of claim 6, further incorporating a specifically cleavable linker peptide functionally interposed between the extracellular domain of the TNF receptor polypeptide and the Fc portion.

CLMS(10)

10. The vector of claim 9, where the specifically cleavable linker peptide comprises a thrombin-sensitive linker peptide.

CLMS(11)

11. The vector of claim 6, where the chimeric polypeptide encoding sequence is positioned adjacent to and under the control of an effective promoter.

CLMS(12)

12. The vector of claim 11, where the promoter comprises a prokaryotic promoter, the vector being adapted for expression in a prokaryotic host.

CLMS(13)

13. The vector of claim 11, where the promoter comprises a eukaryotic promoter, the vector being adapted for expression in a eukaryotic host, and the vector further includes a polyadenylation signal position 3' of the carboxy-terminal amino acid, and within a transcriptional unit of the encoding polypeptide.

CLMS(14)

14. The vector of claim 13, where the eukaryotic promoter comprises a cytomegalovirus promoter.

CLMS(15)

15. The recombinant host cell which incorporated an isolated DNA segment in accordance with claim 1.

CLMS(16)

16. The recombinant host cell of claim 15, further defined as a eukaryotic host cell.

CLMS(17)

17. The recombinant host cell of claim 16, further defined as a CHO cell.

CLMS(18)

18. The recombinant host cell of claim 15, further defined as a prokaryotic host cell.

CLMS(19)

19. The recombinant host cells of claim 15 where the DNA segment encoding a chimeric polypeptide is under the transcriptional control of regulatory signals functional in the recombinant host cell which regulatory signals appropriately control the expression of the chimeric polypeptide in a manner to allow all necessary transcriptional and post transcriptional modification.

CLMS(20)

20. A method of producing a chimeric polypeptide comprising the extracellular domain of the TNF receptor polypeptide functionally attached to a Fc portion and hinge region of an IgG heavy chain polypeptide, the method comprising:

(a) producing a recombinant host cell according to claim 5, such cell

- being capable of expressing the polypeptide;
- (b) culturing the host cell under conditions appropriate for expressing the polypeptide; and
- (c) recovering the chimetic polypeptide.

CLMS (21)

21. The method of claim 20, where additional steps comprise:
- (a) cleaving the polypeptide at the specifically cleavable linker peptide; and
 - (b) recovering the polypeptide comprising an extracellular domain of the TNF receptor polypeptide.

CLMS (22)

22. The method of claim 20 wherein the host cell is a eukaryotic cell.

CLMS (23)

23. The method of claim 22 wherein the eukaryotic cell is a CHO cell.

CLMS (24)

24. The method of claim 22 wherein the eukaryotic cell is an insect cell.

CLMS (25)

25. The method of claim 20 wherein the host cell is a prokaryotic cell.

US PAT NO: 5,426,177 [IMAGE AVAILABLE] L1: 2 of 3
DATE ISSUED: Jun. 20, 1995
TITLE: Ciliary neurotrophic factor receptor
INVENTOR: Samuel Davis, New York, NY
Stephen P. Squinto, Irvington, NY
Mark E. Furth, Pelham, NY
George D. Yancopoulos, Briarcliff Manor, NY
ASSIGNEE: Regeneron Pharmaceuticals, Inc., Tarrytown, NY (U.S. corp.)
APPL-NO: 07/676,647
DATE FILED: Mar. 28, 1991
ART-UNIT: 182
PRIM-EXMR: Robert J. Hill, Jr.
ASST-EXMR: Sally P. Teng
LEGAL-REP: Pennie & Edmonds

US PAT NO: 5,426,177 [IMAGE AVAILABLE] L1: 2 of 3

ABSTRACT:

The present invention relates to the ciliary neurotrophic factor (CNTF) receptor, and provides for CNTF receptor nucleic acid and amino acid sequences. It also relates to (i) assay systems for detecting CNTF activity; (ii) experimental model systems for studying the physiologic role of CNTF; (iii) diagnostic techniques for identifying CNTF-related neurologic conditions; (iv) therapeutic techniques for the treatment of CNTF-related neurologic and muscular conditions, and (v) methods for identifying molecules homologous to CNTF and CNTFR.

CLAIMS:

CLMS(1)

What is claimed is:

1. Isolated and purified CNTF receptor comprising the amino acid sequence as depicted in FIG. 2 (SEQ ID no. 1)

US PAT NO: 5,171,837 [IMAGE AVAILABLE] L1: 3 of 3
DATE ISSUED: Dec. 15, 1992
TITLE: Peptide capable of binding interleukin 6 and an adsorbent
comprising the peptide immobilized on a carrier
INVENTOR: Masao Tanihara, Kurashiki, Japan
Kiichiro Oka, Kurashiki, Japan
ASSIGNEE: Kuraray Co., Ltd., Okayama, Japan (foreign corp.)
APPL-NO: 07/582,831
DATE FILED: Oct. 5, 1990
ART-UNIT: 184
PRIM-EXMR: Robert A. Wax
ASST-EXMR: Stephen Walsh
LEGAL-REP: Wegner, Cantor, Mueller & Player

US PAT NO: 5,171,837 [IMAGE AVAILABLE] L1: 3 of 3

ABSTRACT:

A peptide being capable of binding to interleukin 6, and an adsorbent for interleukin 6 comprising the peptide immobilized on a carrier.

CLAIMS:

CLMS(1)

What is claimed is:

1. A peptide being capable of binding to interleukin 6 represented by the general formula:

H-X-A-Y-Z

wherein A is a peptide segment selected from the group consisting of
a peptide segment of the formula: -Gly-Thr-Val-His-Leu-Leu-Val-Asp-Val-Pro-Pro-Glu-Glu-Pro-Gln-Leu-Ser-Cys-Phe-Arg-Lys-,
a peptide segment of the formula: -Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-Phe-Gln-Glu-Pro-Cys-Gln-Tyr-Ser-Gln-Glu-Ser-,
a peptide segment of the formula: -Thr-Ser-Leu-Pro-Gly-Asp-Ser-Val-Thr-Leu-Thr-Cys-Pro-Gly-Val-Glu-Pro-Glu-Asp-,
a peptide segment of the formula: -Gln-Ala-Leu-Thr-Thr-Asn-Lys-Asp-Asp-Asp-Asn-Ile-Leu-Phe-Arg-Asp-Ser-Ala-,
a peptide segment of the formula: -Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-,
a peptide segment of the formula: -Ser-Thr-Pro-Ser-Leu-Thr-Thr-Lys-Ala-Val-Leu-Leu-Val-Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-,
a peptide segment of the formula: -Asn-Pro-Arg-Trp-Leu-Ser-Val-Thr-Trp-Gln-Asp-Pro-His-Ser-,
a peptide segment of the formula: -His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-

Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys,
a peptide segment of the formula: -Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-,
a peptide segment of the formula: -Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-,
a peptide segment of the formula: -Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-, and
a peptide segment of the formula: -Trp-Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-;
each of X and Y is a single bond or an amino acid residue selected from the group consisting of Asp, Glu, Lys, Ala and a divalent group of the formula: -NH(CH₂)_n-CO- (wherein n is an integer of 1 to 17),
or a peptide segment composed of 2 to 10 amino acid residues selected from the above group bound to each other through a peptide bond; and Z is a hydroxyl group or an amino group.

CLMS (2)

2. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Gly-Thr-Val-His-Leu-Leu-Val-Asp-Val-Pro-Pro-Glu-Glu-Pro-Gln-Leu-Ser-Cys-Phe-Arg-Lys-.

CLMS (3)

3. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-Phe-Gln-Glu-Pro-Cys-Gln-Tyr-Ser-Gln-Glu-Ser-.

CLMS (4)

4. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Thr-Ser-Leu-Pro-Gly-Asp-Ser-Val-Thr-Leu-Thr-Cys-Pro-Gly-Val-Glu-Pro-Glu-Asp-.

CLMS (5)

5. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Gln-Ala-Leu-Thr-Thr-Asn-Lys-Asp-Asp-Asp-Asn-Ile-Leu-Phe-Arg-Asp-Ser-Ala-.

CLMS (6)

6. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys.

CLMS (7)

7. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Ser-Thr-Pro-Ser-Leu-Thr-Thr-Lys-Ala-Val-Leu-Leu-Val-Arg-Lys-Phe-Gln-Asn-Ser-Pro-Ala-Glu-Asp-.

CLMS (8)

8. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Asn-Pro-Arg-Trp-Leu-Ser-Val-Thr-Trp-Gln-Asp-Pro-His-Ser-.

CLMS (9)

9. A peptide according to claim 1, wherein A is a peptide segment of the formula: -His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys.

CLMS(10)

10. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS(11)

11. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS(12)

12. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS(13)

13. A peptide according to claim 1, wherein A is a peptide segment of the formula: -Trp-Gln-Asp-Pro-His-Ser-Trp-Asn-Ser-Ser-Phe-Tyr-Arg-Leu-Arg-Phe-Glu-Leu-Arg-Tyr-Arg-Ala-Glu-Arg-Ser-Lys-.

CLMS(14)

14. An adsorbent comprising the peptide according to claim 1 immobilized on a carrier.

CLMS(15)

15. An adsorbent comprising the peptide according to claim 2 immobilized on a carrier.

CLMS(16)

16. An adsorbent comprising the peptide according to claim 3 immobilized on a carrier.

CLMS(17)

17. An adsorbent comprising the peptide according to claim 4 immobilized on a carrier.

CLMS(18)

18. An adsorbent comprising the peptide according to claim 5 immobilized on a carrier.

CLMS(19)

19. An adsorbent comprising the peptide according to claim 6 immobilized on a carrier.

CLMS(20)

20. An adsorbent comprising the peptide according to claim 7 immobilized on a carrier.

CLMS(21)

21. An adsorbent comprising the peptide according to claim 8 immobilized on a carrier.

CLMS(22)

22. An adsorbent comprising the peptide according to claim 9 immobilized on a carrier.

CLMS(23)

23. An adsorbent comprising the peptide according to claim 10 immobilized on a carrier.

CLMS(24)

24. An adsorbent comprising the peptide according to claim 11 immobilized on a carrier.

CLMS(25)

25. An adsorbent comprising the peptide according to claim 12 immobilized on a carrier.

CLMS(26)

26. An adsorbent comprising the peptide according to claim 13 immobilized on a carrier.

```
=> ds
'DS' IS NOT A RECOGNIZED COMMAND
=> d his
      (FILE 'USPAT' ENTERED AT 10:35:38 ON 03 JUL 96)
L1      3 S HUMAN INTERLEUKIN 6 RECEPTOR?
=> s interleukin 6 receptor?
      2317 INTERLEUKIN
      1835874 6

      23249 RECEPTOR?
L2      12 INTERLEUKIN 6 RECEPTOR?
      (INTERLEUKIN(W) 6(W) RECEPTOR?)
=> s antibod?
L3      19922 ANTIBOD?
=> s l3 and l2
L4      12 L3 AND L2
=> d 1-12
```

1. 5,476,774, Dec. 19, 1995, Quantitation of nucleic acids using the polymerase chain reaction; Alice M. Wang, et al., 435/91.2, 6, 320.1; 536/24.33; 935/77, 78 [IMAGE AVAILABLE]

2. 5,470,730, Nov. 28, 1995, Method for producing T.sub.H -independent

cytotoxic T lymphocytes; Phillip D. Greenberg, et al., 435/172.3; 424/93.21; 435/69.1, 69.52, 70.4, 252.3, 320.1 [IMAGE AVAILABLE]

3. 5,462,731, Oct. 31, 1995, Use of IL-6 for the treatment of chronic lymphocyte leukemia (CLL) and B-cell lymphomas; Dan Aderka, et al., 424/85.2, 85.1; 514/12, 21; 530/351 [IMAGE AVAILABLE]

4. 5,447,851, Sep. 5, 1995, DNA encoding a chimeric polypeptide comprising the extracellular domain of TNF receptor fused to IgG, vectors, and host cells; Bruce A. Beutler, et al., 435/69.7, 69.5, 240.2, 320.1; 530/300, 351; 536/23.4 [IMAGE AVAILABLE]

5. 5,426,177, Jun. 20, 1995, Ciliary neurotrophic factor receptor; Samuel Davis, et al., 530/395, 350, 839 [IMAGE AVAILABLE]

6. 5,326,559, Jul. 5, 1994, Treatment of accelerated atherosclerosis with interleukin-2 receptor targeted molecules; D. Douglas Miller, 424/85.2, 144.1, 183.1; 435/69.5, 69.52, 69.7, 70.21; 514/2, 8, 21, 824; 935/106, 107, 109 [IMAGE AVAILABLE]

7. 5,223,611, Jun. 29, 1993, DNA encoding for human GP130 protein; Tadimitsu Kishimoto, 530/351; 435/69.1, 320.1; 536/23.5 [IMAGE AVAILABLE]

8. 5,219,727, Jun. 15, 1993, Quantitation of nucleic acids using the polymerase chain reaction; Alice M. Wang, et al., 435/6, 91.2, 91.21; 536/24.33; 935/77, 78 [IMAGE AVAILABLE]

9. 5,216,128, Jun. 1, 1993, IFN-.beta.2/IL-6 receptor its preparation and pharmaceutical compositions containing it; Daniela Novick, et al., 530/350, 351, 413, 416, 834 [IMAGE AVAILABLE]

10. 5,188,828, Feb. 23, 1993, Interleukin-6 to stimulate erythropoietin production; Mark A. Goldberg, et al., 424/85.2; 514/8, 12; 530/351 [IMAGE AVAILABLE]

11. 5,171,837, Dec. 15, 1992, Peptide capable of binding interleukin 6 and an adsorbent comprising the peptide immobilized on a carrier; Masao Tanihara, et al., 530/324, 325, 326, 810 [IMAGE AVAILABLE]

12. 5,132,403, Jul. 21, 1992, Human gp130 protein; Tadimitsu Kishimoto, 530/351, 350, 388.22 [IMAGE AVAILABLE]

=>

> d his

(FILE 'USPAT' ENTERED AT 10:35:38 ON 03 JUL 96)

L1 3 S HUMAN INTERLEUKIN 6 RECEPTOR?

L2 12 S INTERLEUKIN 6 RECEPTOR?

L3 19922 S ANTIBOD?

L4 12 S L3 AND L2

=>

THE 1ST DEP. INTERNAL MED., NATL. DEFENCE MED. COLL., 3-2 NAMIKI, *Get*
TOKOROZAWA, SAITAMA 359, JAPAN
CLIN EXP IMMUNOL 88 (1). 1992 75-83. CODEN: CEXIA
Full Journal Title: Clinical and Experimental Immunology
Language: ENGLISH

Introducing avidin-biotin complex ELISA for anti-DNA antibody, the mechanism of in vitro production of anti-ssDNA antibody as well as of polyclonal immunoglobulin mediated by an IL-6-IL-6R loop was studied in patients with systemic lupus erythematosus (SLE). Regardless of the presence or absence of T cells, B cells from SLE patients could produce IgG anti-ssDNA antibody as well as total IgG without any stimulation. Low density B cells obtained by Percoll gradient density centrifugation responded to rIL-6 to produce IgG and IgG anti-ssDNA antibody. rIL-2 and rIL-4 had lesser effects on the differentiation of low density B cells. In fact, IL-6R was preferentially expressed on low density B cells from active SLE patients, as detected by anti-IL-6R MoAb, MT18, which did not inhibit IL-6 binding. SLE B cells, especially high density B cells, produced greater amounts of IL-6 in culture supernatants than did T cells, regardless of whether disease was active or inactive. Normal T cells and B cells did not produce significant amounts of IL-6. Thus, endogenous IL-6 produced by high density B cells bound to the IL-6R preferentially expressed on the low density B cells, and drove them into terminal differentiation, especially in active SLE patients. Further, addition of polyclonal anti-IL-6 or anti-IL-6R MoAb (PM1), which inhibited IL-6 binding, both inhibited IgG anti-ssDNA antibody as well as total IgG production by SLE B cells in a dose-dependent manner. These results suggest that interruption of the autocrine IL-6 loop would be of therapeutic value in SLE.]

16/7/6
DIALOG(R) File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

9032401 BIOSIS Number: 93017401
ANTI-MURINE IL-6 RECEPTOR ANTIBODY INHIBITS IL-6 EFFECTS IN-VIVO
SUZUKI H; YASUKAWA K; SAITO T; ANZAI M; GOITSUKA R; HASEGAWA A; OHSUGI Y;
TAGA T; KISHIMOTO T
INSTITUTE MOLECULAR CELLULAR BIOLOGY, OSAKA UNIV. 1-3, YAMADAOKA,
SUITA-SHI, OSAKA 565, JAPAN.
IMMUNOL LETT 30 (1). 1991 17-22. CODEN: IMLED
Full Journal Title: Immunology Letters
Language: ENGLISH

Thrombopoiesis, as well as antibody production, is one of the major events in which interleukin-6 (IL-6) has been reported to be involved. Polyclonal antimurine IL-6 receptor antibody was prepared to examine the effect of the antibody on these events in IL-6-treated mice. Administration of the anti-mIL-6R antibody inhibited the IL-6-induced increase in the number of platelets. Enhancement of the serum level of DNP-specific antibody by intraperitoneal injection of IL-6 was inhibited completely with simultaneous administration of the anti-mIL-6R antibody. The level of DNP-specific antibody was decreased, even below the basal value, by the higher dose of anti-mIL-6R antibody, indicating its effect also on endogenous IL-6. This work provides evidence that anti-IL-6R antibody inhibits IL-6 function in vivo, and provides an animal model of the therapeutic use of anti-IL-6R antibody for IL-6-related disease.]

File 55:BIOSIS PREVIEWS(R) 1985-1996/Jun W4
(c) 1996 BIOSIS

Set	Items	Description
---	-----	-----
?s il6		
S1	622	IL6
?s receptor?		
S2	301812	RECEPTOR?
?s interleukin(w)6		
	78222	INTERLEUKIN
	621520	6
S3	12338	INTERLEUKIN(W) 6
?ds		

Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?
S3	12338	INTERLEUKIN(W) 6
?s s1 or s3		

	622	S1
	12338	S3
S4	12505	S1 OR S3
?s s4 and s2		

	12505	S4
	301812	S2
S5	2087	S4 AND S2
?s antibod?		

S6	259799	ANTIBOD?
?s s5 and s6		

	2087	S5
	259799	S6
S7	463	S5 AND S6
?s il(w)6r		

	43566	IL
	1245	6R
S8	173	IL(W) 6R
?s s6 and s8		

	259799	S6
	173	S8
S9	64	S6 AND S8
?ds		

Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?

S3 12338 INTERLEUKIN(W) 6
 S4 12505 S1 OR S3
 S5 2087 S4 AND S2
 S6 259799 ANTIBOD?
 S7 463 S5 AND S6
 S8 173 IL(W) 6R
 S9 64 S6 AND S8
 ?s interleukin(w) 6(w) receptor?

78222 INTERLEUKIN
 621520 6
 301812 RECEPTOR?
 S10 281 INTERLEUKIN(W) 6(W) RECEPTOR?
 ?s s6 and s10

259799 S6
 281 S10
 S11 63 S6 AND S10
 ?s s9 or s11

64 S9
 63 S11
 S12 99 S9 OR S11
 ?s py=(1993:1996)

S13 1717319 PY=(1993:1996)
 ?s s12 not s13

99 S12
 1717319 S13
 S14 25 S12 NOT S13
 ?s neutrali? or inhibit?

19962 NEUTRALI?
 468055 INHIBIT?
 S15 483053 NEUTRALI? OR INHIBIT?
 ?s s14 and s15

25 S14
 483053 S15
 S16 12 S14 AND S15
 ?t s16/7/1-12

16/7/1
 DIALOG(R) File 55:BIOSIS PREVIEWS(R)
 (c) 1996 BIOSIS. All rts. reserv.

10029465 BIOSIS Number: 95029465
 ROLE OF INTERLEUKIN 6 IN THE GROWTH OF MYELOMA-DERIVED CELL LINES
 BARUT B A; ZON L I; COCHRAN M K; PAUL S R; CHAUHAN D; MOHRBACHER A;
 FINGEROTH J; ANDERSON K C
 DIV. TUMOR IMMUNOL., DANA-FARBER CANCER INST., 44 BINNEY ST., BOSTON,
 MASS. 02115.
 LEUK RES 16 (10). 1992. 951-959. CODEN: LERED
 Full Journal Title: Leukemia Research
 Language: ENGLISH
 The role of interleukin 6 (IL-6) in the growth of five multiple

myeloma-derived cell lines was characterized. The U266 and RPMI 8226 cells lines demonstrated increased DNA synthesis when cultured with exogenous IL-6, expressed IL-6 cell surface receptors (IL-6Rs) and expressed mRNA for IL-6R. However, these cells did not secrete detectable IL-6 protein, and a neutralizing antibody to IL-6 did not inhibit their growth. Three other myeloma-derived cells lines ARH-77, IM-9 and HS-Sultan did not respond to exogenous IL-6, secrete IL-6 or express cell surface IL-6Rs. The IL-6 responsive cell lines bore late B-cell surface antigens (Ags), CD38 and PCA-1, whereas those lines which were non-IL-6 responsive strongly expressed B1 (CD20) and B4 (CD19) Ags, representing earlier stages in B-cells differentiation. Finally, the two IL-6 responsive cell lines did not express Epstein-Barr virus (EBV) proteins; in contrast, EBV encoded proteins typically expressed during latency could be detected in the three non-IL-6 responsive lines, confirming infection with virus. These studies clarify the heterogeneity observed in the myeloma cell line phenotype and biology and suggest that the U266 and RPMI 8226 cells lines, which express IL-6 cell surface receptors and are IL-6 responsive, may be useful for further study of IL-6 signal transduction in and related IL-6 mediated growth of myeloma in vivo. In contrast, those cell lines which are IL-6-independent provide a model for further study of EBV transformation and IL-6-dependent growth mechanisms in malignancy.

16/7/2

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

9787030 BIOSIS Number: 44037030

CLINICAL APPLICATIONS OF IL6 INHIBITORS

KLEIN B; LU Z Y; BATAILLE R

LAB. D'ONCOGENESE IMMUNOHEMATOL., INST. DE BIOL., 9 QUAI MONCOUSU, 44035
NANTES, FR.

RES IMMUNOL 143 (7). 1992. 774-776. CODEN: RIMME

Full Journal Title: Research in Immunology

Language: ENGLISH

16/7/3

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

9593256 BIOSIS Number: 94098256

ANTI-HUMAN INTERLEUKIN-6 RECEPTOR ANTIBODY INHIBITS HUMAN MYELOMA GROWTH
IN-VIVO

SUZUKI H; YASUKAWA K; SAITO T; GOITSUKA R; HASEGAWA A; OHSUGI Y; TAGA T;
KISHIMOTO T

DEP. MED. III, OSAKA UNIV. MED. SCH., 1-1-50 FUKUSHIMA, FUKUSHIMA-KU,
OSAKA 553, JPN.

EUR J IMMUNOL 22 (8). 1992. 1989-1993. CODEN: EJIMA

Full Journal Title: European Journal of Immunology

Language: ENGLISH

Myeloma is one of the interleukin (IL)-6-related diseases to which abnormal expression of IL-6 has been reported to be linked. We examined the in vivo inhibitory effect of anti-human IL-6 receptor (IL-6R) antibody on human myeloma cell growth in mice. SCID mice were subcutaneously inoculated with solid tumor of the myeloma cell line S6B45 in which human IL-6 was acting as an autocrine growth factor. Ten intraperitoneal administrations of 100 .mu.g of the anti-human IL-6R antibody PM1 at 48-h intervals

strongly inhibited the growth of S6B45 cells when the administration started 24 h after tumor inoculation. The tumor growth inhibition in vivo was also observed by administration of the anti-human IL-6 antibody MH166 using the same procedure as for PM1. The inhibitory effect of PM1 was not significant when the administration started 5 or more days after tumor inoculation. This work indicates that anti-human IL-6R antibody, as well as anti-human IL-6 antibody inhibits human myeloma growth in vivo, and provides an animal model for testing the therapeutic value of agents such as antibodies to human IL-6, IL-6R and gp130, an IL-6R-associated signal transducer, in the treatment of human myelomas.

16/7/4

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

9547472 BIOSIS Number: 94052472

INCREASE IN INTERLEUKIN 6 IL-6 AND IL-6 RECEPTOR EXPRESSION IN A HUMAN MULTIPLE MYELOMA CELL LINE U-266 DURING LONG-TERM IN-VITRO CULTURE AND THE DEVELOPMENT OF A POSSIBLE AUTOCRINE IL-6 LOOP

JERNBERG-WIKLUND H; PETTERSSON M; CARLSSON M; NILSSON K

LAB. TUMOR BIOLOGY, DEP. PATHOLOGY, UNIV. HOSP., S-751 85 UPPSALA, SWEDEN.

LEUKEMIA (BASINGSTOKE) 6 (4). 1992. 310-318. CODEN: LEUKE

Language: ENGLISH

A human multiple myeloma (MM) cell line, U-266, has developed the ability to grow independently of exogenous interleukin 6 (IL-6) during long-term cultivation in vitro. The early passage, feeder-cell dependent U-266 cell line (U-266-1970) was compared with the late passage U-266-1984 cell line with respect to response to IL-6, IL-1.beta. and tumour necrosis factor .alpha. and expression of IL-6 and IL-6 receptor (IL-6R) mRNA and protein. The results showed that; (a) only the U-266-1970 cell line was stimulated to growth by IL-6, (b) IL-6 and IL-6R mRNA were expressed in both cell lines, (c) the level of IL-6 mRNA was increased in the U-266-1984 cell line and only this line produced IL-6 and, (d) the level of IL-6R mRNA was highest in the U-266-1984 cell line and the number of IL-6R about ten times higher than in U-266-1970. The growth of the IL-6-producing U-266-1984 cell line was inhibited by 30% by anti-IL-6R antibodies suggesting the possibility that an autocrine IL-6 loop might have developed during the long-term cultivation. In addition to many other phenotypic alterations of the U-266 cell line, having developed as a consequence of tumor progression in vitro, its growth factor requirement seems to have evolved from a dependence on IL-6 as a paracrine growth factor to a capacity for autonomous growth, dependent on autocrine IL-6 stimulation. Whether such a development also may take place in MM clones in vivo remains to be established.

16/7/5

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

9500353 BIOSIS Number: 94005353

AUTOSTIMULATORY EFFECTS OF IL-6 ON EXCESSIVE B CELL DIFFERENTIATION IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS ANALYSIS OF IL-6 PRODUCTION AND IL-6R EXPRESSION

KITANI A; HARA M; HIROSE T; HARIGAI M; SUZUKI K; KAWAKAMI M; KAWAGUCHI Y; HIDAKA T; KAWAGOE M; NAKAMURA H

16/7/7

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

8588351 BIOSIS Number: 92053351

PREPARATION OF SOLUBLE MURINE IL-6 RECEPTOR AND ANTI-MURINE II-6 RECEPTOR
ANTIBODIES

SAITO T; YASUKAWA K; SUZUKI H; FUTATSUGI K; FUKUNAGA T; YOKOMIZO C;
KOISHIHARA Y; FUKUI H; OHSUGI Y; ET AL

DIV. IMMUNOL., INST. MOL. CELL. BIOL., OSAKA UNIV., 1-3 YAMADA-OKA,
SUITA-SHI, OSAKA 565, JPN.

J IMMUNOL 147 (1). 1991. 168-173. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

Starting with a previously isoalted cDNA clone encoding murine IL-6R, a stable transformed Chinese hamster ovary cell line constitutively expressing soluble murine IL-6R (smIL-6R) has been established. The smIL-6R was purified to homogeneity by sequential filtration and chromatography of culture medium. The smIL-6R augmented the sensitivity of M1 cells to IL-6 in their growth inhibition in a dose-response manner. Rat hybridomas producing mAb specific to murine IL-6R were also established. One of the clones, RS13, produced IgG2a isotype that was capable of inhibiting IL-6 activity. ELISA for the quantitation of smIL-6R was established, which could detect smIL-6R in a quantity as low as 1 ng/ml.

16/7/8

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

8564429 BIOSIS Number: 92029429

IL-6 AND TUMOR NECROSIS FACTOR-ALPHA AUTOCRINE AND PARACRINE CYTOKINES
INVOLVED IN B CELL FUNCTION

RIECKMANN P; D'ALESSANDRO F; NORDAN R P; FAUCI A S; KEHRL J H

LAB. IMMUNOREGULATION, NATIONAL INST. ALLERGY INFECTIOUS DISEASES, NIH,
BUILDING 10, ROOM 11 B 13, BETHESDA, MD. 20892.

J IMMUNOL 146 (10). 1991. 3462-3468. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

IL-6 and TNF-.alpha. are synthesized and secreted by normal tonsillar B cells after stimulation with the polyclonal B cell activator Staphylococcus aureus Cowan strain 1 (SAC) and IL-2 as well as spontaneously by in vivo activated B cells from patients with hypergammaglobulinemia. Using specific neutralizing antibodies, both factors were shown to be involved in autocrine and/or paracrine regulation of B cell differentiation. IgG induced by SAC/IL-2 stimulation was reduced 73% with an anti-IL-6 antibody and 40% with an anti-TNF-.alpha. antibody. Similar effects of these antibodies were observed on the spontaneous in vitro IgG production by lymphoblastic B cells from six patients with hypergammaglobulinemia. Kinetic studies with SAC/IL-2-activated B cells revealed that the anti-TNF-.alpha. antibody must be present at the beginning of the culture to exert an effect on Ig production, whereas the anti-IL-6 antibody reduced Ig production even if added as late as day 3. This sequential action of TNF-.alpha. and IL-6 on B cell differentiation was reflected by different kinetics of release of these two cytokines into the supernatant of SAC/IL-2 activated B cells; TNF-.alpha. peaked at 24 h and IL-6 at 96 h after stimulation. In addition, it was shown that IL-6 production by in vitro-activated B cells was partially blocked by an anti-TNF-.alpha.

antibody suggesting that TNF-.alpha. regulates IL-6 production in normal B cells via an autocrine pathway. We also investigated the effects of TGF-.beta. on TNF-.alpha. and IL-6 production by normal B cells. Although TGF-.beta. inhibited Ig production by in vitro-activated and in vivo-activated B cells, it did not inhibit the release of these cytokines from normal B cells. Furthermore, TGF-.beta. did not inhibit the induction of nuclear factor-IL-6 nor the expression of IL-6R on activated B cells. Thus, although the biologic effects of anti-IL-6 and TGF-.beta. on B cell Ig production are similar, their mechanisms of actions appear to be distinct.

16/7/9

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

8209434 BIOSIS Number: 91130434

CYTOKINE REGULATION OF LOCALIZED INFLAMMATION INDUCTION OF ACTIVATED B CELLS AND IL-6-MEDIATED POLYCLONAL IGG AND IGA SYNTHESIS IN INFLAMED HUMAN GINGIVA

KONO Y; BEAGLEY K W; FUJIHASHI K; MCGHEE J R; TAGA T; HIRANO T; KISHIMOTO T; KIYONO H

DEP. ORAL BIOLOGY, UNIVERSITY ALABAMA BIRMINGHAM, UAB STATION, BIRMINGHAM, ALA. 35294.

J IMMUNOL 146 (6). 1991. 1812-1821. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

It is well established that increased numbers of plasma cells occur in the localized tissues of chronic inflammatory diseases such as adult periodontitis, and enzymatic isolation has shown that most B lineage cells produce IgG-subclass with some IgA-subclass responses. It would be of importance to determine if excess production of cytokines in the localized lesion account for these responses and in the present study we have assessed gingival mononuclear cell (GMC) supernatants for cytokines that activate B cells including IL-6R expression and for levels of IL-6 present. Inasmuch as limited numbers (.apprx.1 to 3 .times. 10⁶ cells) of GMC were obtained from surgically removed tissues (.apprx. 400 mg), we have focused on the analysis of IL-6 production by GMC in this study. Further, initial evidence of additional cytokines that are produced by GMC and induce expression of IL-6R on resting B cells has been obtained. The GMC and PBMC from individual patients were cultured in the presence (or absence) of Con A. Higher levels of IL-6 were produced spontaneously by GMC when compared with Con A-stimulated PBMC. When PBMC cultures were supplemented with GMC supernatants obtained from the same patient, high numbers of spot-forming cells (SFC), mainly in IgG followed by IgA isotype, were seen. The induction of SFC by GMC supernatants was inhibited by incubation with a goat anti-human IL-6 antibody. When the effect of GMC supernatants on subclasses of PBMC SFC was determined, the response was IgG1 > IgG2 > IgG3 = IgG4 and IgA1 > IgA2, a pattern remarkably similar to the distribution of plasma cells in the GMC itself. To assess for cytokines in GMC supernatants that mediated B cell activation, supernatants containing anti-IL-6 were cultured with PBMC or purified B cells for 72 h. This treatment induced small proliferative B cell responses and elevated expression of IL-6R on B cells, but did not induce SFC responses. Further, incubation of B cells with GMC supernatants induced resting B cells (G0/G1) to enter the cell cycle (S and G2/M). Addition of human rIL-6 to these cultures on day 3 restored IgG- and IgA-subclass SFC responses by day 7. Cytokine-induced IL-6R expression also occurred in vivo because freshly isolated GMC

expressed high levels of this receptor. These results show that GMC produce cytokines that induce B cell activation including IL-6R expression and secrete IL-6 that regulates B cell terminal differentiation into plasma cells of IgG- and IgA-subclasses. We are currently assessing the cytokines produced by GMC that induce the expression of IL-6R on B cells.

16/7/10

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

8119517 BIOSIS Number: 91040517

INTERLEUKIN-6 IL-6 IS AN INTERMEDIATE IN IL-1-INDUCED PROLIFERATION OF LEUKEMIC HUMAN MEGAKARYOBLASTS

BRACH M A; LOWENBERG B; MANTOVANI L; SCHWULERA U; MERTELSMANN R; HERRMANN F

DEP. HEMATOLOGY ONCOLOGY, UNIVERSITY FREIBURG MEDICAL CENTER, HUGSTETTERSTRASSE 55, D-7800 FREIBURG, GER.

BLOOD 76 (10). 1990. 1972-1979. CODEN: BLOOA

Full Journal Title: Blood

Language: ENGLISH

We have examined the in vitro effects of recombinant human (rh) interleukin-1 (IL-1) on the growth of purified megakaryoblasts obtained from patients with acute megakaryoblastic leukemia. We demonstrate that both IL-1 alpha and IL-1 beta treatment of these cells led to stimulation of DNA synthesis (as shown by increase of 3H-thymidine incorporation up to 35-fold) and also resulted in colony formation of leukemic megakaryoblasts. However, the stimulatory effect of IL-1 was dependent on endogenous production of IL-6, because addition of neutralizing monoclonal antibody (MoAb) to IL-6 abrogated the stimulatory activity of IL-1. In contrast, neutralizing MoAbs to granulocyte (G)-colony stimulating factor (CSF), granulocyte-macrophage (GM)-CSF, and macrophage (M)-CSF failed to counteract the growth-enhancing effects of IL-1. Leukemic megakaryoblasts accumulated IL-6 mRNA and released IL-6 protein into their culture supernatant when exposed to rh IL-1 but failed to disclose transcripts for G-, GM-, and M-CSF under these conditions. Analysis of IL-6 receptor (IL-6R) transcript levels demonstrated that megakaryoblasts constitutively expressed IL-6R mRNA and that these transcripts are down-regulated to undetectable levels upon exposure to IL-1 and IL-6. Increase of 3H-thymidine incorporation by megakaryoblasts could be duplicated by exogenous IL-6 that could be blocked by neutralizing MoAb to IL-6. In conclusion, our results suggest that leukemic megakaryoblasts could produce and secrete IL-6, and express IL-6R, and that the growth-enhancing effect of IL-1 on these cells is indirect, via production of IL-6 by leukemic cells.

16/7/11

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

7743486 BIOSIS Number: 90111486

ASSOCIATION BETWEEN IL-6 AND CD40 SIGNALING IL-6 INDUCES PHOSPHORYLATION OF CD-40 RECEPTORS

CLARK E A; SHU G

REG. PRIMATE RES. CENT. SJ-50, CENT HEALTH SCI., UNIV. WASHINGTON, SEATTLE, WA 98195.

J IMMUNOL 145 (5). 1990. 1400-1406. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

CD40 mAb at subsaturating doses inhibit the growth of transformants of the M12 murine cell line expressing intact full length CD40 molecules (M12/CD40+ cells) but do not inhibit the growth of two M12 transformants expressing either a mutant CD40 cDNA missing most of the cytoplasmic tail (CD40/tailless) or a mutant cDNA with a substitution at residue 234 (CD40/23A, Ala for Thr). Using these transformants, we tested a panel of cytokines for the ability to mimic CD40 mAb. rIL-6 behaved like CD40 mAb and inhibited the growth of M12/CD40+ cells but not of CD40/tailless or CD40/234A mutants. The effect of IL-6 on M12/CD40+ cells not only required intact CD40 including threonine 234 but also was specific because IL-6 mAb blocked the inhibitory activity. The M12/CD40+ cells responsive to IL-6 expressed > 300,000 CD40 molecules/cells but, like M12/CD40-controls, expressed only small numbers (<50/cell) of high affinity IL-6R, indicating that CD40 is not a receptor for IL-6. Nevertheless, IL-6 utilizes intact CD40 efficiently when it signals these cells: treatment of M12/CD40+ cells with IL-6 induced increased phosphorylation of CD40. Conversely, triggering CD40 on M12/CD40+ cells leads to IL-6 production. Similar effects were evident in human CD40+ B cells: IL-6 increased the phosphorylation of CD40 in the IL-6-responsive cell line, CESS, and CD40 mAb induced IL-6 production in activated human B cells. Thus, CD40 may function to receive and regulate IL-6-dependent signals in B cells.

16/7/12

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

7364057 BIOSIS Number: 89015076

CHARACTERIZATION OF IL-6 RECEPTOR EXPRESSION BY MONOCLONAL AND POLYCLONAL ANTIBODIES

HIRATA Y; TAGA T; HIBI M; NAKANO N; HIRANO T; KISHIMOTO T

DIV. IMMUNOL., INST. MOL. CELL. BIOL., OSAKA UNIV., 1-3 YAMADA-OKA,

SUITA, OSAKA 565, JPN.

J IMMUNOL 143 (9). 1989. 2900-2906. CODEN: JOIMA

Full Journal Title: Journal of Immunology

Language: ENGLISH

mAb and polyclonal antibodies against human IL-6R were prepared by using a murine transfectant cell line expressing the human IL-6R and a synthetic oligopeptide made on the basis of the deduced amino acid sequence as immunogens. Immunoprecipitation of radiolabeled IL-6R with these antibodies showed that the Mr of a mature IL-6R was 80 kDa and its value was reduced to 50K after treatment with O- and N-glycanase and neuraminidase, indicating that IL-6R is a glycoprotein. Two mAb recognizing different epitopes were prepared. One, PM1 inhibited the binding of 125I-IL-6 to the receptor and blocked the IL-6-dependent growth of a T lymphoma line, KT3. PM1 could not bind to IL-6R when it was saturated with IL-6, indicating that this antibody recognizes the IL-6 binding or the adjacent site on IL-6R. The other, MT18 was not inhibited by IL-6R, therefore, this could be used for cytofluorometric staining of normal cells. Nonstimulated B cells expressed undetectable amount of IL-6R regardless of the expression of surface IgD. However, after the stimulation with PWM, IL-6R was observed on IgD- B cells with a relatively large size, but subtly on IgD- small B cells and not on IgD+ B cells, fitting the function of IL-6 which acts on activated B cells to induce Ig production. In contrast, IL-6R was detected on non-stimulated CD4+/CD8- and CD4-/CD8+ T cells. The level of IL-6R on both T cell subpopulations was not significantly changed after stimulation

with phytohemagglutinin.
?s human(w)il(w)6(w)receptor?

```
      2371757  HUMAN
      43566   IL
      621520   6
      301812  RECEPTOR?
S17      30   HUMAN(W) IL(W) 6 (W) RECEPTOR?
```

?ds

Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?
S3	12338	INTERLEUKIN(W) 6
S4	12505	S1 OR S3
S5	2087	S4 AND S2
S6	259799	ANTIBOD?
S7	463	S5 AND S6
S8	173	IL(W) 6R
S9	64	S6 AND S8
S10	281	INTERLEUKIN(W) 6 (W) RECEPTOR?
S11	63	S6 AND S10
S12	99	S9 OR S11
S13	1717319	PY=(1993:1996)
S14	25	S12 NOT S13
S15	483053	NEUTRALI? OR INHIBIT?
S16	12	S14 AND S15
S17	30	HUMAN(W) IL(W) 6 (W) RECEPTOR?

?s s6 and s17

```
      259799  S6
      30      S17
S18      13   S6 AND S17
?s chimeric or humaniz? or reshap?
```

```
      8485   CHIMERIC
      442   HUMANIZ?
      185   RESHAP?
S19      9024 CHIMERIC OR HUMANIZ? OR RESHAP?
?s s18 and s19
```

```
      13     S18
      9024   S19
S20      1   S18 AND S19
?t s20/7/1
```

20/7/1
DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

11039162 BIOSIS Number: 97239162

Humanization of a mouse anti-human interleukin-6 receptor antibody
comparing two methods for selecting human framework regions

Sato K; Tsuchiya M; Saldanha J; Koishihara Y; Ohsugi Y; Kishimoto T;
Bendig M M

Chugai Pharm. Co. Ltd., Fuji-Gotemba Res. Labs, 1-135 Komakado,

Gotemba-shi, Shizuoka 412, JAP

Molecular Immunology 31 (5). 1994. 371-381.

Full Journal Title: Molecular Immunology

ISSN: 0161-5890

Language: ENGLISH

Print Number: Biological Abstracts Vol. 097 Iss. 011 Ref. 156275

Mouse monoclonal antibody AUK12-20 binds to human IL-6 receptor and inhibits IL-6 functions. It has been humanized by CDR-grafting for therapeutic use. In the design of reshaped human AUK12-20 V-L region, the human framework regions (FRs) from the human Bence-Jones protein REI were used. The reshaped human AUK12-20 light chain, in combination with chimeric AUK12-20 heavy chain, bound to antigen as well as chimeric AUK12-20 antibody. In the design of reshaped human AUK12-20 V-H region, two sets of the human FRs were chosen and compared. One set was from the consensus amino acid sequence for human V-H regions subgroup (HSG)-I and the other set was from human antibody HAX, the most similar human V-H region found in a database of human immunoglobulin sequences. The HSG-I-based and the HAX-based reshaped human AUK12-20 heavy chains in combination with the reshaped human AUK12-20 light chain, showed approximately 90 and 100% antigen-binding and competition-binding activities as compared to the chimeric or mouse AUK12-20 heavy chains. Most importantly, these humanized antibodies inhibited the IL-6-dependent tumor cell growth as well as the original mouse antibody suggesting that these humanized antibodies could be efficacious in human patients. Our results show that both approaches for the design of reshaped human antibodies can be used for successful humanization. The approach based on FRs from the most similar individual human antibody, however, seemed to be best for designing a reshaped human antibody that mimicked as closely as possible the original mouse antibody.

?ds

Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?
S3	12338	INTERLEUKIN(W) 6
S4	12505	S1 OR S3
S5	2087	S4 AND S2
S6	259799	ANTIBOD?
S7	463	S5 AND S6
S8	173	IL(W) 6R
S9	64	S6 AND S8
S10	281	INTERLEUKIN(W) 6 (W) RECEPTOR?
S11	63	S6 AND S10
S12	99	S9 OR S11
S13	1717319	PY=(1993:1996)
S14	25	S12 NOT S13
S15	483053	NEUTRALI? OR INHIBIT?
S16	12	S14 AND S15
S17	30	HUMAN(W) IL(W) 6 (W) RECEPTOR?
S18	13	S6 AND S17
S19	9024	CHIMERIC OR HUMANIZ? OR RESHAP?
S20	1	S18 AND S19

?s s10 and s6 and s19

	281	S10
	259799	S6
	9024	S19
S21	2	S10 AND S6 AND S19

?t s21/7/1-2

21/7/1

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

11039162 BIOSIS Number: 97239162

Humanization of a mouse anti-human interleukin-6 receptor antibody
comparing two methods for selecting human framework regions

Sato K; Tsuchiya M; Saldanha J; Koishihara Y; Ohsugi Y; Kishimoto T;
Bendig M M

Chugai Pharm. Co. Ltd., Fuji-Gotemba Res. Labs, 1-135 Komakado,
Gotemba-shi, Shizuoka 412, JAP

Molecular Immunology 31 (5). 1994. 371-381.

Full Journal Title: Molecular Immunology

ISSN: 0161-5890

Language: ENGLISH

Print Number: Biological Abstracts Vol. 097 Iss. 011 Ref. 156275

Mouse monoclonal antibody AUK12-20 binds to human IL-6 receptor and inhibits IL-6 functions. It has been humanized by CDR-grafting for therapeutic use. In the design of reshaped human AUK12-20 V-L region, the human framework regions (FRs) from the human Bence-Jones protein REI were used. The reshaped human AUK12-20 light chain, in combination with chimeric AUK12-20 heavy chain, bound to antigen as well as chimeric AUK12-20 antibody. In the design of reshaped human AUK12-20 V-H region, two sets of the human FRs were chosen and compared. One set was from the consensus amino acid sequence for human V-H regions subgroup (HSG)-I and the other set was from human antibody HAX, the most similar human V-H region found in a database of human immunoglobulin sequences. The HSG-I-based and the HAX-based reshaped human AUK12-20 heavy chains in combination with the reshaped human AUK12-20 light chain, showed approximately 90 and 100% antigen-binding and competition-binding activities as compared to the chimeric or mouse AUK12-20 heavy chains. Most importantly, these humanized antibodies inhibited the IL-6-dependent tumor cell growth as well as the original mouse antibody suggesting that these humanized antibodies could be efficacious in human patients. Our results show that both approaches for the design of reshaped human antibodies can be used for successful humanization. The approach based on FRs from the most similar individual human antibody, however, seemed to be best for designing a reshaped human antibody that mimicked as closely as possible the original mouse antibody.

21/7/2

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

10110788 BIOSIS Number: 95110788

RESHAPING A HUMAN ANTIBODY TO INHIBIT THE INTERLEUKIN 6-DEPENDENT TUMOR
CELL GROWTH

SATO K; TSUCHIYA M; SALDANHA J; KOISHIHARA Y; OHSUGI Y; KISHIMOTO T;
BENDIG M M

FUJI-GOTEMBA RESEARCH LAB., CHUGAI PHARMACEUTICAL CO. LTD., 1-135
KOMAKADO, GOTEMBA, SHIZUOKA 412, JPN.

CANCER RES 53 (4). 1993. 851-856. CODEN: CNREA

Full Journal Title: Cancer Research

Language: ENGLISH

The mouse PM-1 monoclonal antibody binds to the human interleukin 6

receptor, inhibits IL-6 functions, and shows strong antitumor cell activity against multiple myeloma cells. In order to be effective as a therapeutic agent administered to human patients in repeated doses, reshaped human PM-1 antibodies consisting of human REI-based light chain and NEW-based heavy chain variable regions were designed and constructed with the assistance of a structural model of the mouse PM-1 variable regions. The best reshaped human PM-1 antibody is equivalent to mouse or chimeric PM-1 antibody in terms of antigen binding and growth inhibition against multiple myeloma cells. Only a few minor changes in the human framework regions were required to recreate the mouse PM-1 antigen-binding site within a human antibody. The reshaped human PM-1 antibody, therefore, could be efficacious in human multiple myeloma patients.

?s pm(w)1

21795 PM
1252383 1
S22 278 PM(W)1
?s s6 and s22

259799 S6
278 S22
S23 24 S6 AND S22
?t s23/7/1-23

23/7/1
DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

12222771 BIOSIS Number: 98822771

Purification and characterization of salivary kallikrein from an insectivore (*Scalopus aquaticus*): Substrate specificities, immunoreactivity and kinetic analyses

Richards G P; Zintz C; Chao J; Chao L
Med. Univ. South Carolina, Dep. Biochemistry Molecular Biol., 171 Ashley Ave., Charleston, SC 29425, USA

Archives of Biochemistry and Biophysics 329 (1). 1996. 104-112.

Full Journal Title: Archives of Biochemistry and Biophysics

ISSN: 0003-9861

Language: ENGLISH

Print Number: Biological Abstracts Vol. 101 Iss. 012 Ref. 173193

We report the successful one-step separation of tissue kallikrein from the salivary glands of an insectivore, the Eastern Atlantic mole (*Scalopus aquaticus*) by perfusion chromatography. Purified mole salivary kallikrein was characterized as a 30-kDa serine proteinase with a pI of 5.3 and a pH optimum of 9.0. It was readily recognized by human tissue kallikrein antibody in immunoblot analyses. It preferentially hydrolyzes fluorogenic peptidyl substrates with arginyl residues, rather than lysyl residues at the P1 substrate recognition site, indicating that it is like other mammalian kallikreins. Mole kallikrein efficiently releases kinin from low molecular weight human, dog, and bovine kininogen substrates with specific activities similar to that of human tissue kallikrein. Steady state kinetics performed with the synthetic tripeptidyl substrates, Phe-Phe-Arg-, Pro-Phe-Arg-, and Val-Leu-Arg-7-amino-4-methylcoumarin, gave K-m values for mole kallikrein of 3.3, 46.1, and 2.8 μ M, respectively, and specificity constants, k-cat/K-m, of 3818, 165, and 8714 s⁻¹ pM⁻¹, respectively. Mole kallikrein, when compared with human and rat tissue kallikreins, more closely resembles human kallikrein based on immunoreactivity and

kininogenase activity. Mole kallikrein appears to be a member of a single gene or small multigene family. *S. aquaticus* is recommended for studying the evolution of mammalian proteins and may offer advantages over rodent models for biomedical research.

23/7/2

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

12032670 BIOSIS Number: 98632670

Two consecutive nucleotide substitutions resulting in the T3 receptor beta gene resulting in an 11-amino acid truncation in a patient with generalized resistance to thyroid hormone

Miyoshi Y; Nakamura H; Sasaki S; Tagami T; Misaki T; Konishi J; Nakao K
2nd Div., Dep. Internal Med., Hamamatsu Univ. Sch. Med., 3600 Hamadacho,
Hamamatsu 431-31, Japan

Molecular and Cellular Endocrinology 114 (1-2). 1995. 9-17.

Full Journal Title: Molecular and Cellular Endocrinology

ISSN: 0303-7207

Language: ENGLISH

Print Number: Biological Abstracts Vol. 101 Iss. 004 Ref. 048415

We identified unusual mutations in the T3 receptor (TR) beta gene in a 6-year-old Japanese girl with generalized resistance to thyroid hormone. Two consecutive base substitutions, T to A and C to A at nucleotide positions 1637 and 1638, respectively, changed the 451st codon coding for Phe(TTC) to stop codon (TAA), resulting in an 11-amino acid carboxyl(C)-terminus truncation. The patient was a heterozygote. Western blotting using an anti-TR antibody demonstrated the truncated receptor protein. The patient showed severe mental retardation (IQ41), disturbance in speech development, and attention deficit hyperactivity disorder. Thyroid functional status by clinical evaluation was considered within the normal range in spite of high serum thyroid hormone levels (T4 725.9 nmol/l, T3 12.7 nmol/l, FT4 166.0 pmol/l). TSH increased from 0.6 to 24 mU/L after TRH (150 mu-g) injection. TSH secretion as well as 123I-uptake was suppressed only partially by T3 (75 mu-g/day for a week). Close examination of thyroid functions and TR-beta gene analysis were not possible in the family, except for paternal grandmother and one of her two sisters who showed no abnormality. The patient's truncated TR-beta showed very low T3 binding activity ($K_a = 0.1$ times 10^{-10} M), transcriptional activity, and a very strong dominant negative effect. When co-expressed with wild-type TR-beta at the molar ratio 1:1 in CV-1 cells, the mutant receptor inhibited the wild-type TR-beta transcriptional activity by 74% at 10 nM T3. Even 1 mu-M T3 could not normalize these impaired functions.

23/7/3

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

11772862 BIOSIS Number: 98372862

The regulatory site of functional GTP binding protein coupled to the high affinity cholecystokinin receptor and phospholipase A-2 pathway is on the G-beta subunit of G-q protein in pancreatic acini

Tsunoda Y; Owyang C

Dep. Internal Med., Univ. Mich., Ann Arbor, MI 48109, USA

Biochemical and Biophysical Research Communications 211 (2). 1995.

648-655.

Full Journal Title: Biochemical and Biophysical Research Communications

ISSN: 0006-291X

Language: ENGLISH

Print Number: Biological Abstracts Vol. 100 Iss. 005 Ref. 064700

A non-hydrolysable guanosine nucleotide analog, GTP(S) at 200 μ M, stimulated amylase secretion which was inhibited by an anti-phospholipase A-2 (PLA-2) antibody in permeabilized pancreatic acini, indicating that the PLA-2 pathway is linked to the GTP binding protein. A high affinity cholecystokinin (CCK) receptor agonist, CCK-OPE (10 μ M), and a low affinity receptor agonist, CCK-8 (0.1 μ M), both caused amylase secretion in permeabilized cells. The action of CCK-OPE was abolished by the GB antibody but not by the G- α -q,11 antibody, whereas the opposite was true of the CCK-8 response. Biscoclaurine alkaloid isotetrandrine (10 μ M), a specific inhibitor of PLA-2-coupled G proteins, abolished Ca-2+ oscillations and amylase secretion induced by CCK-OPE (0.1100 nM), but not by CCK-8 (10 pM) in intact acini. Gp antagonist-2A (10 μ M), which inhibits the activation of Gq, also inhibited the actions of CCK-OPE (10 pM-1 μ M) in intact acini. These observations indicate that the functional unit of the heterotrimeric G protein coupled to the high affinity CCK receptor appears to be different from that linked to the low affinity CCK receptor/G-q- α pathway. The regulatory site of this G protein coupled to the high affinity CCK receptor is on the beta subunit of G-q protein which elicits Ca-2+ oscillations and monophasic amylase secretion via the PLA-2 pathway.

23/7/4

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

11490979 BIOSIS Number: 98090979

Subclinical hypothyroidism resulting from autoimmune thyroiditis in female patients with endogenous depression

Custro N; Scafidi V; Lo Baido R; Nastri L; Abbate G; Cuffaro M P; Gallo S ; Vienna G; Notarbartolo A

Cattedra di Patologia Medica, Via del Vespro 141, 90127 Palermo, Italy

Journal of Endocrinological Investigation 17 (8). 1994. 641-646.

Full Journal Title: Journal of Endocrinological Investigation

ISSN: 0391-4097

Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 005 Ref. 061389

Thyroid function and presence of thyroid autoantibodies were assessed in a group of 75 consecutive female patients with mood disturbances and in a group of 38 healthy women of similar age recruited as controls. Nine patients suffered from major (endogenous) depression and 66 from minor (neurotic) depression. The individual patients had normal values of circulating thyroid hormones. Nevertheless, endogenously depressed patients had total serum triiodothyronine (M \pm SE=1.49 \pm 0.09 nmol/l) and both total (83.9 \pm 4.3 nmol/l) and free serum thyroxine (13.9 \pm 1.1 pmol/l) lower than in the group of minor depressed and in the group of controls (p \leq 0.01, in both comparison). The median value of serum thyrotropin was 5.22 mU/l in the major depressed patients versus 1.72 mU/l in the minor depressed and 1.69 mU/l in the controls. Thyroid function test results in the minor depressed group did not significantly differ from those in the controls. Five of the 9 endogenously depressed patients were subclinically hypothyroid, while none of the 66 patients with minor depressive disorder showed thyroid dysfunction. Antibodies against thyroglobulin and/or thyroid peroxidase were positive in all the 5 endogenously depressed women with

subclinical hypothyroidism, revealing a symptomless autoimmune thyroiditis, which was also confirmed by ultrasonography in all cases and histopathologically demonstrated in one case. None of the endogenously depressed women without thyroid dysfunction and none of the 66 minor depressives were seropositive for thyroid autoantibodies. Only one of the non-depressed women in the control group was found seropositive for TPO-Ab and showed an exaggerated TSH responsiveness to TRH stimulation. The findings indicate the possibility that endogenous depression is accompanied by latent hypothyroidism in an appreciable proportion of women. The detection of thyroid autoantibodies in such patients suggests that affective disorders might play a precipitating role in the development of thyroid autoimmune disease. Therefore, the possibility of immunological damage should be taken into consideration whenever depressed women display biochemical thyroid dysfunction.

23/7/5

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

11413460 BIOSIS Number: 98013460

Transforming growth factor beta 2 is the predominant isoform in the neural retina, retinal pigment epithelium-choroid vitreous of the monkey eye

Pfeffer B A; Flanders K C; Guerin C J; Danilepour D; Anderson D H
Storz Div. American Cyanamid, Build. 96, Room 225A, 401 N. Middletown
Road, Pearl River, NY 10965, USA

Experimental Eye Research 59 (3). 1994. 323-333.

Full Journal Title: Experimental Eye Research

ISSN: 0014-4835

Language: ENGLISH

Print Number: Biological Abstracts Vol. 099 Iss. 001 Ref. 013460

Several techniques were utilized to assess the levels, disposition and cellular sources of isoforms 1 and 2 of transforming growth factor beta (TGF-beta) in the posterior pole of the monkey eye. Freshly dissected tissues, as well as the saline vehicles in which dissections were performed, were analysed by sandwich enzyme-linked immunosorbent assay. In all tissues TGF-beta-2 was the predominant isoform, with beta-2:beta-1 ratios of 6: 1 for neural retina (as ng g-1) and 425:1 for vitreous (as pmol 1-1). Retinal pigment epithelium (RPE)-Bruch's membrane-choroid complex contained approximately 10 times the amount of both TGF-beta isoforms as neural retina. For first passage cultures of monkey RPE, TGF-beta-2, but not TGF-beta-1, accumulated over time in conditioned media samples. Immunoreactivity for TGF-beta-2 was detected both in tissue sections of posterior pole, specifically in rod outer segments and RPE, and also in the first passage cultures of RPE. Antibodies to specific peptide sequences of both isoforms localized TGF-beta to the outer segments of rod photoreceptors. The apparent sequestration of TGF-beta-2 in photoreceptor outer segments, as well as the in vitro evidence for possible synthesis and release by RPE, suggest that TGF-beta-2 is an important modulator of visual function acting at the retina-RPE interface.

23/7/6

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

11249497 BIOSIS Number: 97449497

Cryptic nature of envelope V3 region epitopes protects primary monocytotropic human immunodeficiency virus type 1 from antibody neutralization

Bou-Habib D C; Roderiquez G; Oravec T; Berman P W; Lusso P; Norcross M A
Div. Hematol. Products, Center Biol. Evaluation Res., Food Drug
Administration, NIH, Building 29A, Room 3B10, 8800 Rockville Pike, HFM-541,
Bethesda, MD 20892, USA

Journal of Virology 68 (9). 1994. 6006-6013.

Full Journal Title: Journal of Virology

ISSN: 0022-538X

Language: ENGLISH

Print Number: Biological Abstracts Vol. 098 Iss. 008 Ref. 103809

Characterization of biological and immunological properties of human immunodeficiency virus type 1 (HIV-1) is critical to developing effective therapies and vaccines for AIDS. With the use of a novel CD4+ T-cell line (PM-1) permissive to infection by both monocytotropic (MT) and T-cell-tropic virus types, we present a comparative analysis of the immunological properties of a prototypic primary MT isolate of HIV-1 strain JR-CSF (MT-CSF) with those of a T-cell-tropic variant (T-CSF) of the same virus, which emerged spontaneously in vitro. The parental MT-CSF infected only PM-1 cells and was markedly resistant to neutralization by sera from HIV-1-infected individuals, rabbit antiserum to recombinant MT-CSF gp120, and anti-V3 monoclonal antibodies. The T-CSF variant infected a variety of CD4+ T-cell lines, contained positively charged amino acid substitutions in the gp120 V3 region, and was highly sensitive to antibody neutralization. Neutralization and antibody staining of T-CSF-expressing cells were significantly inhibited by HIV-1 V3 peptides; in contrast, the MT strain showed only weak V3-specific binding of polyclonal and monoclonal antibodies. Exposure of PM-1 cells to a mixture of both viruses in the presence of human anti-HIV-1 neutralizing antiserum resulted in infection with only MT-CSF. These results demonstrate that although the V3 region of MT viruses is immunogenic, the target epitopes in the V3 principal neutralizing domain on the membrane form of the MT envelope appear to be cryptic or hidden from blocking antibodies.

23/7/7

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

10930136 BIOSIS Number: 97130136

Direct and correlated responses to multitrait, divergent selection for immunocompetence

Kean R P; Cahaner A; Freeman A E; Lamont S J

Dep. Animal Sci., Iowa State Univ., Ames, IA 50011, USA

Poultry Science 73 (1). 1994. 18-32.

Full Journal Title: Poultry Science

ISSN: 0032-5791

Language: ENGLISH

Print Number: Biological Abstracts Vol. 097 Iss. 006 Ref. 079999

Leghorn lines had been selected for an immunocompetence index based on four traits: antibody production to Mycoplasma gallisepticum (MG) and Pasteurella multocida (PM) vaccines, reticuloendothelial clearance of colloidal carbon (CCA), and cell-mediated, wing web response to phytohemagglutinin (PHA). The purpose of this study was to produce replicated lines of chickens with divergent levels of multitrait immunocompetence by index selection. The objectives of analyses of Generations 5 to 7 of this study was to characterize these lines with

respect to immune-response traits, correlations among these traits, and correlated responses in other important production traits. Differences (P lt .05) existed between the lines selected for high or low immune response and between the two replicates in mean breeding values and in individual immune-response traits. Averages of heritability estimates, weighted by number of offspring and pooled across three generations (two cycles of selection), estimated by using sire variance components and parent-offspring correlations were, respectively, .16 and .09 for the index, .31 and .08 for MG, .21 and -.02 for PM, .06 and .05 for CCA, and .08 and .12 for PHA. Realized heritabilities (response divided by effective selection differential) pooled across the two selection cycles, were .19 and .11 for the index, .06 and -.01 for MG, .44 and .32 for PM, 1.52 and -1.21 for CCA, and .48 and .15 for PHA, for Replicates 1 and 2, respectively. Phenotypic correlations among traits were generally small, and several estimates were negative. Estimates of genetic correlation varied widely. Juvenile and adult body weights, age of first egg, 32-wk egg weight, and rate of egg production were analyzed to evaluate effects of selection on these traits of direct economic importance. Very few differences were noted.

23/7/8

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

10110788 BIOSIS Number: 95110788

RESHAPING A HUMAN ANTIBODY TO INHIBIT THE INTERLEUKIN 6-DEPENDENT TUMOR CELL GROWTH

SATO K; TSUCHIYA M; SALDANHA J; KOISHIHARA Y; OHSUGI Y; KISHIMOTO T;
BENDIG M M

FUJI-GOTEMBA RESEARCH LAB., CHUGAI PHARMACEUTICAL CO. LTD., 1-135
KOMAKADO, GOTEMBA, SHIZUOKA 412, JPN.

CANCER RES 53 (4). 1993. 851-856. CODEN: CNREA

Full Journal Title: Cancer Research

Language: ENGLISH

The mouse PM-1 monoclonal antibody binds to the human interleukin 6 receptor, inhibits IL-6 functions, and shows strong antitumor cell activity against multiple myeloma cells. In order to be effective as a therapeutic agent administered to human patients in repeated doses, reshaped human PM-1 antibodies consisting of human REI-based light chain and NEW-based heavy chain variable regions were designed and constructed with the assistance of a structural model of the mouse PM-1 variable regions. The best reshaped human PM-1 antibody is equivalent to mouse or chimeric PM-1 antibody in terms of antigen binding and growth inhibition against multiple myeloma cells. Only a few minor changes in the human framework regions were required to recreate the mouse PM-1 antigen-binding site within a human antibody. The reshaped human PM-1 antibody, therefore, could be efficacious in human multiple myeloma patients.

23/7/9

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

10098735 BIOSIS Number: 95098735

DEVELOPMENT OF MONOCLONAL ANTIBODIES SPECIFIC FOR 1 N-2
ETHENODEOXYGUANOSINE AND N-2 3 ETHENODEOXYGUANOSINE AND THEIR USE FOR
QUANTITATION OF ADDUCTS IN G12 CELLS EXPOSED TO CHLOROACETALDEHYDE

FOILES P G; MIGLIETTA L M; NISHIKAWA A; KUSMIEREK J T; SINGER B; CHUNG
F-L
DIV. CHEM. CARCINOGENESIS, AMERICAN HEALTH FOUND., ONE DANA RD.,
VALHALLA, NY 10595, USA.

CARCINOGENESIS (OXF) 14 (1). 1993. 113-116. CODEN: CRNGD

Language: ENGLISH

Monoclonal antibodies specific for N2,3-ethenodeoxyguanosine (N2,3-.epsilon.dGuo) and 1,N2-ethenodeoxyguanosine (1,N2-.epsilon.dGuo) were developed. In a competitive ELISA, 50% inhibition of binding of the N2,3-.epsilon.dGuo specific antibody (ETH1) was achieved with 18 fmol of N2,3-.epsilon.dGuo. Fifty per cent inhibition of the 1,N2-.epsilon.dGuo-specific antibody (ETH2) required 11 pmol 1,N2-.epsilon.dGuo. Immunoassays for N2,3-.epsilon.dGuo and 1,N2-.epsilon.dGuo in single-stranded DNA were developed using these antibodies. The immunoassays could detect as little as 48 fmol of N2,3-.epsilon.dGuo or 340 fmol 1,N2-.epsilon.dGuo in 25 .mu.g of single stranded DNA. These assays and previously developed immunoassays for 1,N6-ethenodeoxyadenosine (1,N6-.epsilon.dAdo) and 3,N4-ethenodeoxycytidine (3,N4-.epsilon.dCyd) were used to measure etheno adduct levels in DNA of cells exposed to chloroacetaldehyde. The cells used were V79 cells with an inactivated hprt gene and a single copy of the bacterial gpt gene (G12 cells). The most abundant etheno adduct was 1,N6-.epsilon.dAdo, followed by 3,N4-.epsilon.dCyd and N2,3-.epsilon.dGuo. 1,N2-.epsilon.dGuo was not detected in chloroacetaldehyde-treated G12 cells. Chloroacetaldehyde was also shown to be mutagenic in these same cells.

23/7/10

DIALOG(R) File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

10020207 BIOSIS Number: 95020207

INCREASED TISSUE CONCENTRATIONS OF THE GASTRIN PRECURSOR IN PATIENTS
TREATED WITH OMEPRAZOLE

NEMETH J; VARRO A; BRIDSON J; WALKER R; DOCKRAY G J

DEP. PHYSIOL., UNIVERSITY LIVERPOOL, CROWN ST., PO BOX 147, LIVERPOOL L69
3BX, UK.

EUR J CLIN INVEST 22 (10). 1992. 638-644. CODEN: EJCIB

Full Journal Title: European Journal of Clinical Investigation

Language: ENGLISH

The main form of gastrin in antral mucosa, the amidated heptadecapeptide G17, is generated from an inactive precursor, progastrin, by steps involving endopeptidase cleavage and amidation. Gastrin cells are normally inhibited by gastric acid and in this study we have examined how suppression of acid by treatment with omeprazole for 6-8 weeks influences gastrin production in patients with oesophagitis. Plasma concentrations of total amidated gastrins in the fasting state increased from 18 to 43 pmol l⁻¹; assays specific for G17-immunoreactivity indicated that the plasma concentrations of this form increased from 6 to 12 pmol l⁻¹. In endoscopic biopsies of antral mucosa there was no change with omeprazole treatment in the concentrations of total amidated gastrins, or their immediate precursors, the Gly-extended gastrins. However, assays using an antibody that reacts with progastrin, together with size exclusion chromatography, indicated that tissue progastrin concentration increased 6-fold. The data suggest a modest net increase in gastrin production with omeprazole-treatment; because the ratio of tissue concentrations of total amidated gastrins to Gly-extended gastrins did not change, it would seem that the amidating capacity of the gastrin cell was maintained. However,

the increase in progastrin concentrations suggests a relative failure of the initial steps of post-translational processing, and consequently that in certain circumstances endopeptidase cleavage of progastrin may be rate limiting.

23/7/11

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

9143686 BIOSIS Number: 93128686

TROPHOBLAST-DERIVED TUMOR NECROSIS FACTOR-ALPHA INDUCES RELEASE OF HUMAN CHORIONIC GONADOTROPIN USING INTERLEUKIN-6 IL-6 AND IL-6-RECEPTOR-DEPENDENT SYSTEM IN THE NORMAL HUMAN TROPHOBLASTS

LI Y; MATSUZAKI N; MASUHIRO K; KAMEDA T; TANIGUCHI T; SAJI F; YONE K; TANIZAWA O

1-1-50 FUKUSHIMA, FUKUSHIMA-KU, OSAKA 553, JPN.

J CLIN ENDOCRINOL METAB 74 (1). 1992. 184-191. CODEN: JCEMA

Full Journal Title: Journal of Clinical Endocrinology & Metabolism

Language: ENGLISH

The titer of tumor necrosis factor-.alpha. (TNF.alpha.) secreted by placental blocks was determined by enzyme immunoassay. The source of placental TNF.alpha. was immunohistochemically demonstrated with monoclonal anti-TNF.alpha. antibody to be only trophoblasts. Purified trophoblasts produced 174.4 ng/L TNF.alpha. by 24 h of culture in vitro. To investigate the role of TNF.alpha. in placental hormonogenesis, purified trophoblasts were stimulated with recombinant TNF.alpha. (rTNF.alpha.) to determine the hCG titer by enzyme immunoassay. Trophoblasts stimulated with rTNF.alpha. released hCG in a dose-dependent fashion with kinetics similar to those of recombinant interleukin-1 (rIL-1)-stimulated trophoblasts. The stimulated trophoblasts released IL-6 before hCG, but failed to show hCG release when pretreated with anti-IL-6 receptor (anti-IL-6R) monoclonal antibody PM-1. However, the pretreatment of trophoblasts with PM-1 did not interfere with rTNF-.alpha.-induced IL-6 release, ruling out the possibility of a nonspecific toxic effect of PM-1 on trophoblasts. These results suggest that trophoblast-derived TNF.alpha. induced IL-6 release and then activated the IL-6 -R system in trophoblasts to release hCG. Since IL-1 has also been demonstrated to induce similar release of IL-6 and hCG from trophoblasts, the effects of TNF.alpha. and IL-1 on these trophoblast functions were also examined. Simultaneous stimulation of trophoblasts with rTNF.alpha. and .gamma.IL-1.alpha. resulted in synergistic enhancement of IL-6 release, subsequently leading to enhanced hCG release. Collectively, trophoblast-derived TNF.alpha. and IL-1 synergistically regulated the level of IL-6 secreted by trophoblasts, the magnitude of which determined the level of hCG released by activating the IL-6-R system in trophoblasts.

23/7/12

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

9113449 BIOSIS Number: 93098449

RADIO-IMMUNOASSAY OF ENDOTHELIN IN HUMAN PLASMA

SORENSEN S S

DEP. NEPHROLOGY MED. C, SKEJBY HOSP., DK-8200 AARHUS C, DENMARK.

SCAND J CLIN LAB INVEST 51 (7). 1991. 615-623. CODEN: SJCLA

Full Journal Title: Scandinavian Journal of Clinical and Laboratory Investigation

Language: ENGLISH

Endothelin (ET) is a newly described endothelium-derived 21-amino-acid peptide with potent vasoconstrictive properties. The present study describes a radio-immunoassay utilizing an antibody without cross-reactivity with big endothelin, produced after immunization of rabbits with endothelin-1 (ET-1). Measurement of endothelin in human plasma was performed after prior extraction on Sep-pak C18 cartridges. Recovery of unlabelled endothelin-1 added to human plasma (3.5 pg ml⁻¹) was 84.8 \pm 11.1% (mean \pm SD, n = 12). The minimum detectable level in plasma was 50 fmol l⁻¹. High-pressure liquid chromatography on reverse-phase C18 column established that the measured irET eluted identically to ET-1. The concentration of irET in plasma from healthy control subjects was 1.11 \pm 0.2 pmol l⁻¹ (mean \pm SD, n = 30). Agarose electrophoresis of plasma with [125I]-ET-1 indicated a reversible binding to albumin. It is concluded that ET-1 is present in measurable amounts in human plasma. It is suggested that ET-1 in plasma is associated with albumin. The importance of an adequate extraction procedure is stressed.

23/7/13

DIALOG(R) File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

9112746 BIOSIS Number: 93097746

DETERMINATION OF PLASMA CHOLECYSTOKININ CCK CONCENTRATIONS BY BIOASSAY AND RADIOIMMUNOASSAY IN MAN A CRITICAL EVALUATION

HOECKER M; SCHMIDT W E; CREUTZFELDT W; CHOUDHURY A R; NUSTEDE R; SCHAFFMAYER A; FOELSCH U R

DIVISION GASTROENTEROLOGY ENDOCRINOLOGY, DEP. MEDICINE, UNIVERSITY HOSPITAL, GEORG-AUGUST-UNIVERSITY GOETTINGEN, ROBERT-KOCH-STRASSE 40, D-3400 GOETTINGEN, GER.

REGUL PEPT 37 (3). 1992. 255-269. CODEN: REPPD

Full Journal Title: Regulatory Peptides

Language: ENGLISH

The present investigation was designed to perform a direct comparison of a rat pancreatic acini bioassay system and a specific CCK radioimmunoassay (antiserum G-160) for the measurement of fasting and meal-stimulated plasma CCK in the presence and absence of the CCK receptor antagonist loxiglumide. The G-160 CCK antiserum is directed against the C-terminal O-sulfated tyrosine residue of the CCK molecule which is essential for full bioactivity of CCK peptides. For plasma extraction prior to bioassay measurement, hydrophobic reverse-phase chromatography on octadecylsilane cartridges was employed and resulted in simultaneous adsorption and elution of both CCK peptides and loxiglumide with recoveries of 87.5 \pm 9% and 75.0 \pm 5.9%, respectively. In the absence of loxiglumide, fasting and meal-stimulated values for CCK-like bioactivity and CCK-immunoreactivity (IR-CCK) were nearly identical (basal values: 1-2 pmol/l; meal-stimulated plateau levels; 4-6 pmol/l). After intravenous infusion of loxiglumide (30 mg/kg/h for 10 min, 10 mg/kg/h thereafter), resulting in plasma steady state levels of 200-300 μ mol/l, meal-stimulated CCK-like bioactivity was undetectable, whereas IR-CCK levels were augmented 6.5-fold. In the bioassay system, standard samples containing 50 μ mol/l loxiglumide produced complete inhibition of acinar lipase release in response to 50 pmol/l synthetic CCK-8. We conclude, that postprandial circulating non-CCK-like factors do not contribute significantly to the direct receptor-mediated stimulation of exocrine pancreatic secretion. The good agreement of CCK-like bioactivity and IR-CCK levels in the absence of loxiglumide confirms the sensitive and specific recognition of bioactive

CCK peptides by the G-160 antiserum and suggests that this antibody exerts binding characteristics probably similar to a pancreatic acinar receptor.

23/7/14

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

9020358 BIOSIS Number: 93005358

EARLY UNDIFFERENTIATED CONNECTIVE TISSUE DISEASE II. THE FREQUENCY OF CIRCULATING ANTINUCLEAR ANTIBODIES IN PATIENTS WITH EARLY RHEUMATIC DISEASES

CLEGG D O; WILLIAMS H J; SINGER J Z; STEEN V D; SCHLEGEL S; ZIMINSKI C; ALARCON G S; LUGGEN M E; POLISSON R P; ET AL

DIV. RHEUMATOL., ROOM 4B 200, UNIV. UTAH MED. CENT., 50 NORTH MEDICAL DRIVE, SALT LAKE CITY, UTAH 84132.

J RHEUMATOL 18 (9). 1991. 1340-1343. CODEN: JRHUA

Full Journal Title: Journal of Rheumatology

Language: ENGLISH

The presence of antinuclear antibodies (ANA) in the serum is a common finding in various connective tissue disorders, but usefulness of these antibodies in making diagnoses or prognoses is not known. We report the results of a panel of ANA determinations including ANA, anti-dsDNA, Sm, RNP, SSA, SSB, Jo-1, Scl-70 and PM-1 in 410 patients in a 5-year descriptive study of 410 patients with rheumatic disease symptoms of less than one year's duration. While some patients met diagnostic criteria for a specific rheumatologic diagnosis, others were classified as undifferentiated connective tissue disease (UCTD) and were subclassified by a constellation of symptoms. Our results show that ANA is sensitive in systemic lupus erythematosus (SLE) and progressive systemic sclerosis even in early disease but is not specific. Other "specific" autoantibodies were seen most frequently in SLE but were relatively insensitive and were seen in low frequency in UCTD. ANA have limited diagnostic value in patients with early disease. The prognostic value of these tests will be assessed as the prospective study of these cohorts progresses.

23/7/15

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

8085593 BIOSIS Number: 91006593

PARADOXICAL ENHANCEMENT OF INTERLEUKIN-2-MEDIATED CYTOTOXICITY AGAINST K562 CELLS BY ADDITION OF A LOW DOSE OF METHOTREXATE

NAKARAI T; UENO Y; UENO Y; KOIZUMI S

DEP. PEDIATRICS, KANAZAWA UNIV. SCH. MED., 13-1 TAKARA-MACHI, KANAZAWA 920, JAPAN.

CANCER IMMUNOL IMMUNOTHER 32 (1). 1990. 8-12. CODEN: CIIMD

Full Journal Title: Cancer Immunology Immunotherapy

Language: ENGLISH

In vitro effects of methotrexate (MTX) on interleukin-2(IL-2)-mediated cytotoxicity of peripheral blood mononuclear cells (PBMC) were studied. PBMC were incubated with human recombinant IL-2 (25 U/ml) for 72 h; during the last 24 h, various concentrations (10 pM-1 μ M) of MTX were added to the culture. Cytotoxicity against k562 cells was measured by a 4-h ⁵¹Cr-release assay. The IL-2-mediated cytotoxicity was paradoxically increased at around a concentration (10 nM) MTX. Such a low concentration of MTX showed no anti-proliferative effect on cell growth. This enhancement

with 10 nM MTX was shown only in an E-rosette+ (E+) population, but not in E-rosette- (E-). In addition, when E+ cells were treated with an anti-CD16 monoclonal antibody plus complement after incubation with IL-2 and MTX, MTX-induced enhancement was lost, suggesting that an E+CD16+ cell population was mainly involved in this augmentation. Positively sorted E+CD16+ cells showed similar enhancement of cytotoxicity after treatment with IL-2 plus MTX. On the other hand, MTX treatment did not show the phenotypical changes including of the E+CD16+ cells, indicating that this treatment did not affect the differentiation and proliferation of the specific cell subset. Our results indicate that a low dose of MTX could have a role in the regulation of immunological anti-cancer surveillance systems through the natural killer and lymphokine-activated cytotoxic cells.

23/7/16

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

7729928 BIOSIS Number: 90097928

TROPHOBLAST-DERIVED INTERLEUKIN-6 IL-6 REGULATES HUMAN CHORIONIC GONADOTROPIN RELEASE THROUGH IL-6 RECEPTOR ON HUMAN TROPHOBLASTS

NISHINO E; MATSUZAKI N; MASUHIRO K; KAMEDA T; TANIGUCHI T; TAKAGI T; SAJI F; TANIZAWA O

DEP. OBSTETRICS GYNECOLOGY, OSAKA UNIVERSITY MEDICAL SCHOOL, 1-1-50 FUKUSHIMA, FUKUSHIMA-KU, OSAKA 553, JPN.

J CLIN ENDOCRINOL METAB 71 (2). 1990. 436-441. CODEN: JCEMA

Full Journal Title: Journal of Clinical Endocrinology & Metabolism

Language: ENGLISH

We examined the capacity of trophoblast-derived interleukin-6 (IL-6) to stimulate secretion of placental hormones, including hCG. IL-6 stimulated hCG secretion by trophoblasts to a level similar to that stimulated by a GnRH analog. The analog, however, released hCG by an IL-6-independent mechanism because PM-1, a monoclonal antibody specific for IL-6 receptors (R), failed to block GnRH-mediated responses, but completely blocked IL-6 mediated hCG secretion, suggesting the existence of two distinct regulatory pathways for hCG release. Immunohistochemical analysis with another IL-6-R-specific antibody, MT-18, showed that IL-6-R was located only on the trophoblast layer of the placenta. Our data revealed the existence of a local regulatory network by which trophoblast-derived IL-6 interacts with IL-6-R on the trophoblasts, resulting in hCG release. Thus, two different regulatory networks, an IL-6 and IL-6-R system and a GnRH and GnRH-R system, regulate hCG release by human trophoblasts independently.

23/7/17

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

7692329 BIOSIS Number: 90060329

MOLECULAR VARIANTS OF CHOLECYSTOKININ AFTER ENDOGENOUS STIMULATION IN HUMANS A TIME STUDY

EYSSELEIN V E; EBERLEIN G A; HESSE W H; SCHAEFFER M; GRANDT D; WILLIAMS R ; GOEBELL H; REEVE J R JR

DEP. GASTROENTEROL., HARBOR-UCLA MED. CENT., 1000 W. CARSON, ST., TORRANCE, CALIF. 90509.

AM J PHYSIOL 258 (6 PART 1). 1990. G951-G957. CODEN: AJPHA

Full Journal Title: American Journal of Physiology

Language: ENGLISH

The time-dependent release of molecular variants of cholecystokinin (CCK) into the circulation was studied before and 1, 2, and 4 h after a test meal in six healthy volunteers. At each time period, 100 ml of blood were drawn in a manner to inhibit CCK degradation. Plasma was formed and CCK concentrated by Sep-Pak C18 cartridge chromatography. Molecular variants of CCK and gastrin were well separated from each other by high-performance liquid chromatography (HPLC). Molecular forms of CCK and gastrin were measured by radioimmunoassay using an antibody that requires the presence of the carboxyl-terminal phenylalanine amide for full recognition, implying that biologically active forms were detected. HPLC elution positions of gastrin forms were determined using a gastrin-specific antibody. Chromatographic separation of CCK from gastrin forms was complete, allowing separate integration of gastrin and CCK forms. Therefore no subtraction of gastrin-like immunoreactivity from CCK-like immunoreactivity (CCK-LI) was necessary and CCK-LI could be directly determined. Peaks of CCK-LI were integrated in the column eluates and the plasma concentrations were calculated. Total plasma CCK-LI rose from a value of 2.4 \pm 0.6 pM before the test meal to 6.4 \pm 0.8, 6.6 \pm 0.9, and 5.8 \pm 1.2 pM 1, 2, and 4 h postprandially. The major molecular forms released into the circulation eluted on HPLC in the position of CCK-58 and CCK-39 (which coelutes with CCK-33). Minor amounts were detected in the position of CCK-8. There was no significant difference in the relative proportions of the molecular forms released at the different time periods. The high proportions of CCK-58 in human plasma indicate that it expresses a major portion of CCK's biological activity.

23/7/18

DIALOG(R) File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

7398030 BIOSIS Number: 89049049

DETECTION AND ANTIGENIC CHARACTERIZATION OF ANTINUCLEAR ANTIBODIES IN CONNECTIVE TISSUE DISEASES

DE MARNEFFE P; MALAISE M; DEFLANDRE E; HAUWAERT C; LALLEMAND M P; FRANCHIMONT P

SERV. RHUMATOLOGIE, CHU SART TILMAN, LIEGE.

REV MED LIEGE 44 (19). 1989. 577-591. CODEN: RMLIA

Full Journal Title: Revue Medicale de Liege

Language: FRENCH

To determine the correlation between the presence of antinuclear antibodies (ANA) and connective tissue disease, a prospective clinical study was conducted on 167 patients with one of the following conditions: systemic lupus erythematosus (SLE), induced lupus, rheumatoid arthritis, scleroderma, mixed connective tissue disease, primary Sjogren's syndrome, dermatomyositis, combined SLE and scleroderma, and psoriatic arthritis. ANA in patients' serum were detected and titrated by indirect immunofluorescence, and the pattern of immunofluorescence (homogeneous, peripheral, speckled, nucleolar, centromeric or chromosomal) was noted; ANA were characterized using the "nDNA C. L. Sci. Medx", "ENA antigen system" and "ANA check" kits from Biolab SA. Serum ANA were found to include antibodies to native DNA (anti-DNA), deoxyribonucleoprotein (anti-DNP), and extractable nuclear antigens (anti-ENA); included in the last group were anti-Smith antibodies (anti-Sm), antibodies to ribonucleoprotein (anti-U1-RNP), and the antibodies to Ro/SS-A, La/SS-B, Scl-70, Jo-1, PM-1, Ku, centromere and nucleolus. Some ANA were found to be specific for certain diseases, e.g. anti-DNA for lupus, anti-Sm for SLE, anti-Scl-70 and

anticentromere for scleroderma. Other antibodies, although not specific, were frequently associated with diseases, e.g. anti-RNP with SLE, anti-Ro/SS-A and anti-La/SS-B with Sjogren's syndrome. Detection and characterization of ANA was concluded to be of prognostic value and could be used as a diagnostic tool and an aid in treatment planning.

23/7/19

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

6944784 BIOSIS Number: 87005305

EFFECT OF INTERLEUKIN 1 BETA ON TRANSDUCING MECHANISMS IN 235-1 CLONAL
PITUITARY CELLS PART II MODULATION OF CALCIUM FLUXES

SCHETTINI G; MEUCCI O; FLORIO T; SCALA G; LANDOLFI E; GRIMALDI M
DEP. PHARMACOL., II SCH. MED., VIA PANSINI 5, 80131 NAPOLI, ITALY.

BIOCHEM BIOPHYS RES COMMUN 155 (3). 1988. 1097-1104. CODEN: BBRCA

Full Journal Title: Biochemical and Biophysical Research Communications

Language: ENGLISH

In the present study we investigated the effect of the interleukin 1 beta on intracellular free calcium concentrations in 235-1 cell line both in basal conditions and after stimulation by the calcium channel activator maitotoxin. Interleukin 1 beta (from 0.01 pM to 10 nM) was unable to significantly affect basal cytosolic free calcium levels in acute conditions. The preincubation of these cells with interleukin 1 beta for 48th modulates maitotoxin stimulation of calcium fluxes without modifying basal intracellular free calcium levels. Low concentrations of interleukin 1 beta (0.01 pM, 1 pM) caused a marked reduction of intracellular free calcium concentrations increase induced by maitotoxin while higher doses of the monokine potentiated maitotoxin stimulation of calcium fluxes. The specificity of interleukin 1 beta effect was tested by means of polyclonal anti-interleukin 1 beta antibody (titer 1:100) which significantly abolished the inhibitory effect of interleukin 1 beta on free cytosolic calcium levels. These results show that a long lasting interaction of interleukin 1 beta with its receptor is able to influence voltage-sensitive calcium channels activation induced by maitotoxin in 235-1 cells.

23/7/20

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

6638080 BIOSIS Number: 86104631

ENHANCED HUMAN MONOCYTE CYTOTOXICITY BY PLATELET-ACTIVATING FACTOR

VALONE F H; PHILIP R; DEBS R J

DEP. MED., VA MED. CENTER, SAN FRANCISCO, CA 94143, USA.

IMMUNOLOGY 64 (4). 1988. 715-718. CODEN: IMMUA

Full Journal Title: Immunology

Language: ENGLISH

The capacity of platelet-activating factor (PAF) to enhance human monocyte cytotoxicity for WEHI 164 cells was examined. Spontaneous monocyte cytotoxicity was 24 .+- . 2% (mean .+- . SEM, n =9). Preincubation of monocytes with 1 pM-1 nM PAF for 18 hr significantly enhanced cytotoxicity in a dose-related manner, whereas less enhancement was observed at PAF concentrations above 1 nM. Maximal PAF-induced cytotoxicity was 68 .+- . 6%, which was similar to that induced by optimal concentrations of tumour necrosis factor (TNF) and interferon-gamma. The specific PAF antagonist kadsurenone inhibited PAF-induced cytotoxicity but not TNF-induced

cytotoxicity. The inactive PAF analogues lysoPAF and enantioPAF did not increase monocyte cytotoxicity. Two observations suggest that TNF mediates PAF-induced cytotoxicity: specific anti-TNF antibodies inhibited PAF induced cytotoxicity toward WEHI 164 cells, and PAF did not enhance cytotoxicity to TNF-resistant cells. PAF represents a distinct class of phospholipid monocyte activators that increase monocyte cytotoxicity by TNF-dependent mechanisms.

23/7/21

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

5427916 BIOSIS Number: 82072719

SMALL NUCLEAR RIBONUCLEOPROTEIN ANTIGENS ARE ABSENT FROM 10S TRANSLATION INHIBITORY RIBONUCLEOPROTEIN BUT PRESENT IN CYTOPLASMIC MESSENGER RIBONUCLEOPROTEIN AND POLYSOMES

BOAK A M; KOVACS S A; AGRIS P F; CHAKRABORTY D; SARKAR S
DEP. MED. DIV. BIOL. SCI., UIV. MISSOURI, COLUMBIA, MO. 65211.
ARCH BIOCHEM BIOPHYS 248 (1). 1986. 89-100. CODEN: ABBIA
Full Journal Title: Archives of Biochemistry and Biophysics
Language: ENGLISH

A cytoplasmic 10S ribonucleoprotein particle (iRNP), which is isolated from chick embryonic muscle, is a potent inhibitor of mRNA translation in vitro and contains a 4S translation inhibitory RNA species (iRNA). The iRNP particle shows similarity in size to the small nuclear ribonucleoprotein (snRNP) particles. Certain autoimmune disease patients contain antibodies directed against snRNP antigenic determinants. The possibility that iRNP may be related to the small nuclear particles was tested by immunoreactivity with monospecific autoimmune antibodies to six antigenic determinants (Sm, RNP, PM-1, SS-A (Ro), SS-B (La), and Scl-70). By Ouchterlony immunodiffusion assays, the cytoplasmic 10S iRNP did not show any immunoreactivity. Also, a more sensitive hemagglutination inhibition assay for detecting Sm and RNP antigens failed to show reactivity with the 10S iRNP. Thus, the 10S iRNP particles are distinct from the similarly sized snRNP. However, free and polysomal messenger ribonucleoprotein (mRNP) particles and polysomes also isolated from chick embryonic muscle and analyzed by Ouchterlony immunodiffusion and hemagglutination inhibition for the presence of the antigenic determinants showed reactivity to Sm and RNP autoantibodies, but were not antigenic for the other four antibodies. Some of the Sm antigenic peptides of mRNP particles and polysomes were identical to those purified from calf thymus nuclear extract, as judged by Western blot analysis. The association of Sm with free and polysomal mRNP and polysomes suggests that Sm may be involved in some cytoplasmic aspects of mRNA metabolism, in addition to a nuclear function in mRNA processing.

23/7/22

DIALOG(R)File 55:BIOSIS PREVIEWS(R)
(c) 1996 BIOSIS. All rts. reserv.

4853405 BIOSIS Number: 79095720

IMMUNOGENETIC STUDIES OF JUVENILE DERMATOMYOSITIS 3. STUDY OF ANTIBODY TO ORGAN-SPECIFIC AND NUCLEAR ANTIGENS

PACHMAN L M; FRIEDMAN J M; MARYJOWSKI-SWEENEY M L; JONNASON O; RADVANY R M; SHARP G C; COBB M A; BATTLES N D; CROWE W E; ET AL
DIV. IMMUNOLOGY/RHEUMATOLOGY, CHILDREN'S MEMORIAL HOSPITAL, 2300
CHILDREN'S PLAZA, CHICAGO, IL 60614.

ARTHRITIS RHEUM 28 (2). 1985. 151-157. CODEN: ARHEA

Full Journal Title: Arthritis and Rheumatism

Language: ENGLISH

Children (90) with definite juvenile dermatomyositis (JDMS), who had been HLA typed, were tested for the presence of tissue or organ-specific antibodies. Sixty had active disease at the time of study. The mean disease duration was 4 yr and 30 had soft tissue calcifications. The following autoantibodies were sought: thyroid, gastric parietal cells, smooth muscle, striated muscle, microsomes, mitochondria, DNA, extractable nuclear antigen, Sm, PM-1, antinuclear antibody (ANA) and rheumatoid factor. Only the ANA and PM-1 were more frequent in patients than in controls ($P < 0.0002$ and $P < 0.001$, respectively). Higher levels of immune complexes ($P < 0.01$) were in sera from patients with JDMS than in sera from controls and were correlated with the presence of ANA in patients ($P < 0.01$). Soft tissue calcification was not associated with any autoantibody or HLA antigen, but with disease duration and activity ($P < 0.001$ and $P < 0.05$, respectively). There was no association between the occurrence of any autoantibody and the presence of HLA-B8 or DR3 among the white patients with JDMS. The frequency of autoantibodies in 43 full siblings of children with JDMS was not increased. Children with JDMS, with or without HLA-B8/DR3, do not show evidence of a generalized nonspecific antibody response to tissue antigens. The significance of the increased antibody to nuclear antigens ANA and PM-1 remains to be determined.

23/7/23

DIALOG(R)File 55:BIOSIS PREVIEWS(R)

(c) 1996 BIOSIS. All rts. reserv.

4836297 BIOSIS Number: 79078612

HIGH-AFFINITY MONOCLONAL ANTIBODIES FOR AFLATOXINS AND THEIR APPLICATION TO SOLID-PHASE IMMUNOASSAYS

GROOPMAN J D; TRUDEL L J; DONAHUE P R; MARSHAK-ROTHSTEIN A; WOGAN G N
BOSTON UNIVERSITY SCHOOL PUBLIC HEALTH, HUBERT H. HUMPHREY CANCER
RESEARCH CENTER, DEPARTMENT MICROBIOLOGY, SCHOOL MEDICINE, 80 EAST CONCORD
STREET, BOSTON, MASS. 02118.

PROC NATL ACAD SCI U S A 81 (24). 1984 (RECD. 1985). 7728-7731.

CODEN: PNASA

Full Journal Title: Proceedings of the National Academy of Sciences of the United States of America

Language: ENGLISH

Monoclonal antibodies specific for aflatoxin B1, aflatoxin B2, aflatoxin M1 and the major aflatoxin-DNA adducts were obtained following fusion of mouse SP-2 myeloma cells with spleen cells of mice immunized with aflatoxin B1 covalently bound to bovine gamma globulin. The aflatoxin-modified protein used to immunize mice was produced chemically by activating aflatoxin B1 to a 2,3-epoxide derivative, which then covalently bound to the protein. One of the monoclonal antibodies isolated (2B11) was a high-affinity IgM antibody with an affinity constant for aflatoxin B1, aflatoxin B2 and aflatoxin M1 of .apprx. 1 .times. 10⁹ l/mol. In a competitive radioimmunoassay using [3H]aflatoxin B1, 3 pmol (1 ng) of aflatoxin B1, aflatoxin B2 or aflatoxin M1 caused 50% inhibition with this antibody. The antibody also had significant cross-reactivity for the major aflatoxin-DNA adducts: 2,3-dihydro-2-(N7-guanyl)-3-hydroxyaflatoxin B1 and 2,3-dihydro-2-(N5-formyl-2',5',6'-triamino-4' oxo-N5-pyrimidyl)-3-hydroxyaflatoxin B1. The antibody was also covalently bound to Sepharose-4B and used in a column-based solid-phase immunosorbent assay system. Aflatoxins added in vitro to phosphate buffer, human urine, human serum or human milk at

levels expected to be obtained in human samples acquired from environmentally exposed individuals were quantitatively recovered by applying the mixture to this antibody affinity column purification system. Preliminary studies using urine samples from rats injected with radiolabeled aflatoxin B1 have also indicated that aflatoxin metabolites can be isolated by these methods. The monoclonal antibody affinity columns can be regenerated for multiple use. Therefore, the monoclonal antibodies and their application to affinity chromatography represents a useful and rapid technique to purify environmentally occurring levels of this carcinogen and some of its metabolites for quantitative measurements.

?

PLEASE ENTER A COMMAND OR BE LOGGED OFF IN 5 MINUTES

?ds

Set	Items	Description
S1	622	IL6
S2	301812	RECEPTOR?
S3	12338	INTERLEUKIN(W) 6
S4	12505	S1 OR S3
S5	2087	S4 AND S2
S6	259799	ANTIBOD?
S7	463	S5 AND S6
S8	173	IL(W) 6R
S9	64	S6 AND S8
S10	281	INTERLEUKIN(W) 6 (W) RECEPTOR?
S11	63	S6 AND S10
S12	99	S9 OR S11
S13	1717319	PY=(1993:1996)
S14	25	S12 NOT S13
S15	483053	NEUTRALI? OR INHIBIT?
S16	12	S14 AND S15
S17	30	HUMAN(W) IL(W) 6 (W) RECEPTOR?
S18	13	S6 AND S17
S19	9024	CHIMERIC OR HUMANIZ? OR RESHAP?
S20	1	S18 AND S19
S21	2	S10 AND S6 AND S19
S22	278	PM(W) 1
S23	24	S6 AND S22

?